

FIG. 1

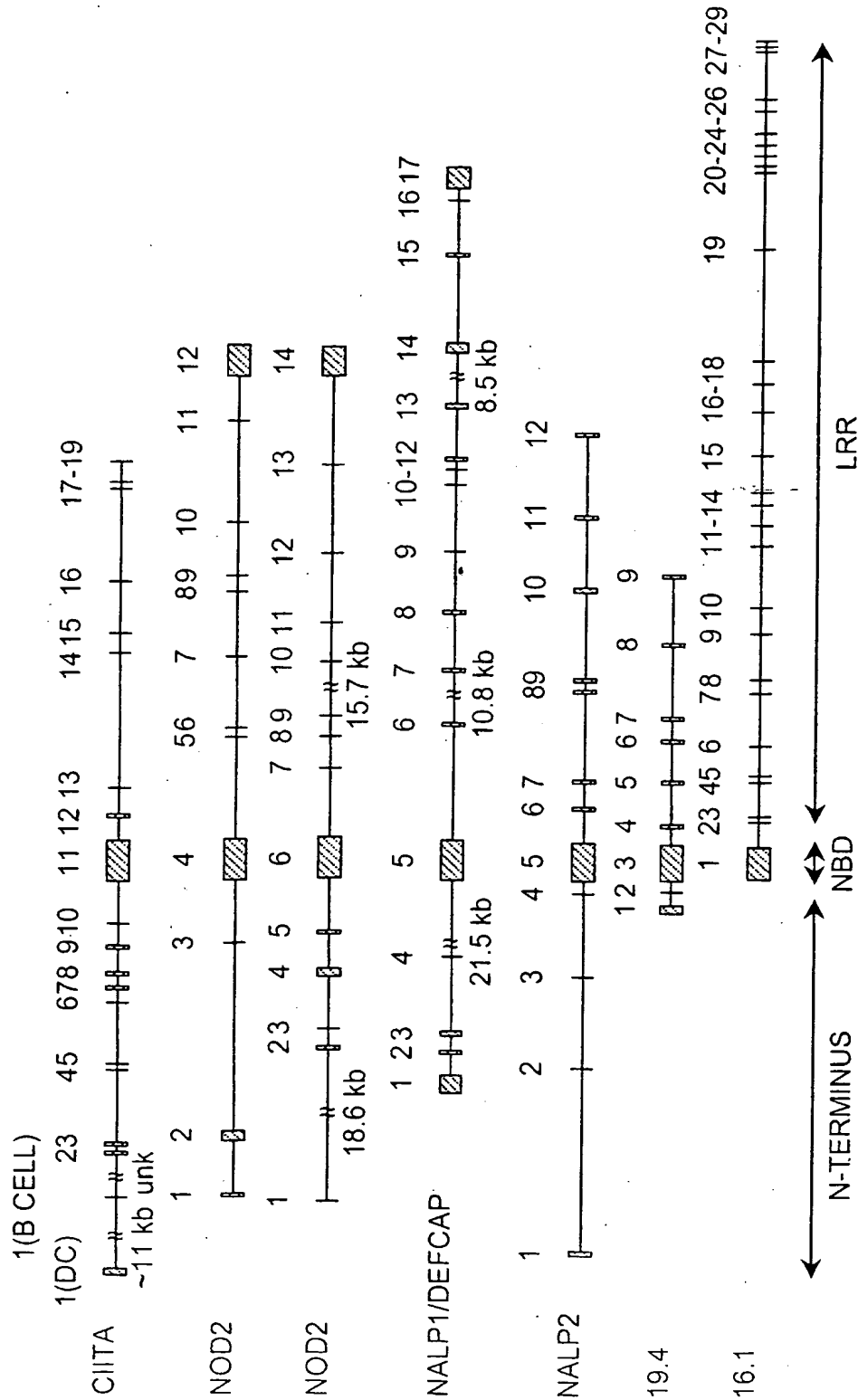


FIG.2A

MOTIF I

-TVVL-G-AGhGKTTLAbbhL-WA-G-Lr (SEQ ID NO:150)
 * * * * *

MOTIF II

F-rhFrh-CbEh-----Sh-aLl---rP (SEQ ID NO:151)
 * * * * *

MOTIF III

-lh--PaRLLFlhDGFDEL (SEQ ID NO:152)
 * * * * *

MOTIF IV

LL-SLLbK-LLPEASLLlTpRP-Ah (SEQ ID NO:153)
 * * * * *

MOTIF V

L--hL---b-h-h-GFSE-abb--YF--r-a (SEQ ID NO:154)

MOTIF VI¹

A-bsh--hb-N--Lr-hC-VP-hCWhVCp-Lb-Qha-G (SEQ ID NO:155)
 * * * * *

MOTIF VII

T-T-hr--rh---h (SEQ ID NO:156)

MOTIF VIII²

Lb-LC-LAAEGhW----hF--aDL---GL----h--FL---hh (SEQ ID NO:157)
 * *

MOTIF IX³

Y-FhHLphQEF-AAhrYhL (SEQ ID NO:158)
 * * * * *

MOTIF X

FLFGLL-(-)n-b-LE--Fs--hS--hb (SEQ ID NO:159)

MOTIF XI

haLF-Clra-QE-aFh---h-----h-h (SEQ ID NO:160)

MOTIF XII

ahhV-pFCLbbC--h--L-L (SEQ ID NO:161)

FIG. 2B

Rec'd PCT/PTO 21 OCT 2004

MOTIF I

		* * * * *	* * * * *	*	*
1.1	MELLFDPDDEHSEPV	HTVVFQGAAGIGK	TILARKMMLDWAS	GTLYQ	
19.3	IETLFEPDEERPEPP	RTVVMQGAAGIGK	SMLAHKVMLDWAD	GKLFQ	
19.1	EYKELNDAYTAAARR	HTVVLEGP	DGIGKTTLLRKVM	LWDWAEGNLWK	
12	-----	-----	-----	-----	
DEFCAP	IRDLFGPGLDTQEP	RIVILQGAAGIGK	STLARQVKEAWGR	GQLYQ	
11.2	LEHLFDVDVKTGAQP	QIVVLQGAAGVGK	TTLVRKAMLDWA	EGSLYQ	
19.5	LDRLFAPKETGKQP	RTVIIQGPQGIGK	TTLMLKLMMAWSD	NKIFR	
19.7	LQRLDPNRTRAQA	QTIVLVGRAGVGK	TTLAMRAMLHWAN	GVLFQ	
19.2	LPCLLLPKRPQGRQP	KTVAIQGAPGIGK	TILAKKVMFEWAR	NKFYA	
11.1	VEALFDSGEKPSLAP	SLVVLQGSAGTGK	TTLARKMVLWDWA	TGTYLP	
Nalp2/19.4	LIPFSNPRVLPGPFS	YTVVLYGPAGLGK	TTLAQKLMLDWA	EDNLIH	
19.8	TLAGAFDSDRWGFRP	RTVVLHGKSGIGK	SALARRIVLCWAQ	GGLYQ	
11.4	TFNRLFRRDEEGRRP	LTVVVLQGPAGIGK	TMAAKKILYDWA	AGKLYQ	
19.6	LQLAYDSTSYYSAAN	LNVLFLMGERASGK	TIVINLAVLRWIK	GEMWQ	
X	-----	-----	-----	-----	
11.3	LSQLFNPDACGRRV	QTVVLYGTVGTGK	STLVRKMVLWDW	CYGRLLPA	
CIITA	EVLLAAKEHRRPRET	RVI AVL GKAGQG	KSYWAGAVSRAW	ACGRLPQ	
16.1	VSISDLFNTRVNKGP	RVTVLLGKAGMGK	TTLAHRLCQKWA	EGHLNC	
16.2	LDRLFPLSRVSVPP	RVSITIGVAGMGK	TTLVRHFVRLWA	HGQVGK	
Nod2	LEELFSTPGHLNDDA	DTVLVVGEGAGSGK	STLLQRLHLLWA	AGQDFQ	
Nod1	ACLLDHTTGILNEQG	ETIFILGDAGVGK	SMLLQRLQSLWA	TGRLLDA	
Ipaf	RVEQLTLNGLLQALQ	SPCII EGESGKGK	STLLQRIAMLWG	SGKCKA	
NAIP	VQEPLVLPFVFGNLN	SVMCVEGEAGSGK	TVLLKKIAFLWA	SGCCPL	

MOTIF II

		* * * * *			
1.1	-DRFDYLFYIHCREVS	---LVTQRS	LGDLIMSCCP	---	DPNPPIH
19.3	-GRFDYLFYINCREMNQ	---SATECS	MQDLIFSCWP	---	EPSAPLQ
19.1	-DRFTFVFFFLNVCEMN	---GIAETS	LLELLSRDWP	---	ESSEKIE
12	-----	-----	-----	-----	
DEFCAP	-DRFQHVFFYFSCRELA	---QSKVVS	LAE LIGKDG	---	ATPAPIR
11.2	-QRFKYVFFYLN GREIN	---QLKERS	FAQLISKDWP	---	STEGPIE
19.5	-DRFLYTFFYFCCREL	---ELPPTS	LADLISREW	---	DPAAPIT
19.7	-QRFSYVFFYLSCHKIR	---YMKETT	FAELISLDWP	---	DFDAPIE
19.2	-HKRWCAFYFHCQEVN	---QTTDQS	FSELIEQKWP	---	GSQDLVS
11.1	-GRFDYVFFYVSCKEVV	---LLESKLE	QLLFWCCG	---	DNQAPVT
Nalp2/19.4	-K-FKYAFYLSCRELS	---RLGPCS	FAELVFRDWP	---	ELQDDIP
19.8	-GMFSYVFFLPVREM	---RKKESS	VTEFISREW	---	DSQAPVT
11.4	-GQVDFAFFMPCGELLE	---RPGTRS	LADLILDQCP	---	DRGAPVP
19.6	-NMISYVVHLTSHEIN	---QMTNSS	LAE LIAKDWP	---	DGQAPIA
X	-GRCDYLIYVNCIEIS	---HIANLS	SADLILTLFK	---	INGPIL
11.3	---FELLIPFSCEDLSS	---LGPAPAS	LCQLVAQRYT	---	PLKEVLP
CIITA	---YDFVFSVPCHCLNR	---PGDAYG	LQDLLFSLGP		QPLVAADDEVFS
16.1	-FQALFLFEFRQLNLIT	---RFLTPS	ELLFDLYLSP	ES--	DHDTV FQ
16.2	-D-FSLVLPLTFRDLN	---THEKLC	ADR LICSVFP	---	HVGEPS
Nod2	-E-FLFVFPFSCRQLQC	---MAKPLS	VRTLLFEHCC		WPDVGQEDIFQ
Nod1	-G-VKFFFHFRCRMFSCFKES	DRCLQDLLFKHYC			YPERDP
Ipaf	LTKFKFVFFLRLSRAQG	---GLFETL	CDQLLDIPGT	---	IRKQTFMA
NAIP	LNRFQLVFYLSLSSTRP	DEGLASI ICDOLLEKEGS		---	VTEMCMRN

FIG. 3A
4/68

MOTIF III

	***	*****	
1.1	KIVRKPSRILFLMDGFDELQ	GAFDEHI ----	GPLCTDWQKAERGD
19.3	ELIRVPERLLFIIDGFDELK	PSFHDPQ ----	GPWCLCWEEKRPTE
19.1	DIFSQPERILFIMDGFEQLK	FNLQLK ----	ADLSDDWRQRQPMP
12	HFFPQPEQILFIMDGFEQLK	FDLELK ----	ADLCDDWRQQQPTQ
DEFCAP	QILSRPERLLFILDGVDEPG	WVLQEPS ----	SELCLHWSQPQPAD
11.2	EIMYQPSSLLFIIDSFDELN	FAFEEPE ----	FALCEDWTQEHVPS
19.5	EIVSQPERLLFVIDSFEELO	GGLNEPD ----	SDLCGDLMEKRPVQ
19.7	EFMSQPEKLLFIIDGFEEII	ISESRSESLDDGSPCTDWYQELPVT	
19.2	KIMSKPDQLLLLLLDGFEELO	STLIDR ----	LEDLSEDWRQKLPGS
11.1	EILRQPERLLFILDGFDELQ	RPFEELK ----	LKKRGLSPKE
Nalp2/19.4	HILAQARKILFVIDGFDELG	AAPGALI ----	EDICGDWEKKKPVP
19.8	EIMSRPERLLFIIDGFDDLQ	SVLNNDT ----	KLCKDWAEKQPPF
11.4	QMLAQQRLLFILDGADELQ	ALGGPE ----	AAPCTDPFEAASGA
19.6	DILSDPKLLFILEDLNIR	FELNVN ----	ESALCSNSTQKVPI
X	DTILIYPKILLILDRFPELO	DPVGDQE ----	EDLSVHPQERRPVE
11.3	LMAAAGSHLLFVLHGLEHLN	LDLRLAG ----	TGLCSDPEEPQEP
CIITA	HILKRPDRVLLILDAFEELE	AQDQGLH ----	STCGPAPAEPCLSR
16.1	YLEKNADQVLLIFDGLDEAL	QPMGPDg ----	PGPVL
16.2	LAVAVPARALLILDGLDECR	TPLDFSN ----	TVACTDPKKEIPVD
Nod2	LLLDHPDRVLLTFDGFDEFK	FRFTDR ----	ERHCS-PTDPTSVQ
Nod1	FLLRFPHVALFTFDGLDELH	SDLDSLRS ----	VPDSSCPWEPAPHL
Ipaf	MLLKLQRVFLLDGYNEFK	PQNC ----	
NAIP	IIQQLKNQVFLLDYKEIC	SIPQ ----	

MOTIF IV

MOTIF V

	* * *	* * *	* * *	* * *	* * *	
1.1	ILLSSLIRKKLLPEASLLITTRPVALEK	LQHLLDHPRHVEILGFS				
19.3	LLNSLIRKKLLPELSLLITTRPTALEK	LHRLLEHPRHVEILGFS				
19.1	IILSSLLQKKMLPESSLLIALGKLAMQK	HYFMLRHPKLIKLLGFS				
12	IILSSLLQKKMIPESLLIALGKVGMQK	NYFMLXHPKLIKLPQFT				
DEFCAP	ALLGSLGKTILPEASFLITARTTALQN	LIPSLQARWVEVLGFS				
11.2	FLMSSLLRKVMLPEASLLVTTTLTTSKR	LKQLLKNHHYVELLGMS				
19.5	VLLSSLLRKKMLPEASLLIAIKPVCPE	LRDQVTISEIYQPRGFN				
19.7	KILHSLKKELVPLATLLITIKTWVFRD	LKASLVNPCFVQITGFT				
19.2	VLLSSLLSKTMLPEATLLIMIRFTSWQT	CKPLLKCPSLVTLPGFN				
11.1	SLHLLIRRHRTLPTCSLLITTRPLALRN	LEPLLKQARHVHILGFS				
Nalp2/19.4	VLLGSLNLRVMLPKAALLVTTTRPRALRD	LRILAEPIYIRVEGFL				
19.8	TLIRSLLRKVLLPESFLIVTVRDVGTEK	LKSEVVSPRYLLVRGIS				
11.4	RVLGGLLSKALLPTALLVTTTRAAAPGR	LQGRLCSPQCAEVRGFS				
19.6	VLLVSLLKRKMAPGCWFLISSRPTRGNN	VKTFLKEVDCCTTLQLS				
X	SLLCSFVRKKLFPESLLITARTPTAMKK	LHSLKQPIQAEILWFT				
11.3	AIIVNLLRKYMPLQASILVTTTRPSAIGR	IPSKY -VGRYGEICGFS				
CIITA	GLLAGLFQKKLLRGCTLLLTARPRG -RL	VQSLSKADALFELSGFS				
16.1	TLFSLCNGTLLPGCRVMATSRPGK --L	PACLPAAEAMVHMLGFD				
16.2	HLITNIIRGNLFPEVSIWITSRPSASGQ	IPGGL -VDRMTEIRGFN				
Nod2	TLLFNLLQGNLLKNARKVVTSRPAVSA	FLRKY -IRTEFNKLGFS				
Nod1	VLLANLLSGKLLKGASKLLTARTGIEVP	RQFLR ---KKVLLRGFS				
Ipaf	PEIEALIKENHRFKNMVIVTTTTECLRH	IRQFGALTAEVGDMTED				
NAIP	-VIGKLIQKNHLSRTCLLIAVRTNRARD	IRRYLETILEIKAFPFY				

MOTIF V

MOTIF VI'

1.1	EAKRKE - YFFKYFSDE	-----A	QARAAFSLI
19.3	EAERKE - YFYKYFHNA	-----E	QAGQVFNYV
19.1	ESEKKS - YFSYFFGEK	-----S	KALKVFNFV
12	ELERKL - YFSYFFSEK	-----N	KALKAFHFV
DEFCAP	ESSRKE - YFYRYFTDE	-----R	QAIRAFRLV
11.2	EDAREE - YIYQFFEDK	-----R	WAMKVFSSSL
19.5	ESDRLV - YFCCFFKDP	-----K	RAMEAFNLV
19.7	GDDLRLV - YFMRHFDDSD	-----S	EVEKILQQL
19.2	TMEKIK - YFQMYFGHT	-----E	EGDQVLSFA
11.1	EEERAR - YFSSYFTDE	-----K	QADRAFDIV
Nalp2/19.4	EEDRRA - YFLRHFGDE	-----D	QAMRAFELM
19.8	GEQRIHLLLERGIGE -	-----H	KMTQGLRAI
11.4	DKDKKK - YFYKFFRDE	-----R	RAERAYRFV
19.6	NGKREI - YFNSFFKDR	-----Q	RASAALQLV
X	DTEKRA - YLLSQFSGA	-----N	TTMKVFDYL
11.3	DTNLQKLYFQLRLNQP	YCGYAVGGSGVSATPAQRDH	LVQMLSRNL
CIITA	MEQAQA - YVMRYFESS	-----GMTE	HQDRALTLL
16.1	GPRVEE - YVNHFFSAQ	-----P	SREGALVEL
16.2	EEEIKVC - LEQMFPED	-----QA	LLGWMLSQV
Nod2	EQGIEL - YLRKRHHEP	-----G	VADRLIRLL
Nod1	PSHLRA - YARRMFPER	-----A	LQDRLLSQL
Ipaf	SAQALIREVLIKELA -	-----	--EGLLLQI
NAIP	NTVCILRKLFSSHMT -	-----	RLRKFMVYF

MOTIF VI'

* * * * *

1.1	QENEVLFTMCFIPLVCWIVCTGLKQQMESGK	SLAQTSK ----
19.3	RDNEPLFTMCFVPLVCWVCTCLQQQLEGGG	LLRQTSR ----
19.1	RDNGPLFILCHNPFTCWLVTCTVKQRLERGE	DLEINSQ ----
12	RDTGQRFILCHNPFTICWLVTCTCMKWQLERGE	DLEINSQNTFI
DEFCAP	KSNKELWALCLVPVWSWLACTCLMQQMKRKE	KLTLTISK ----
11.2	KSNEMLFSCQVPLVCWAACTCLKQQMEKGG	DVTLTCTQ ----
19.5	RESEQLFSICQIPLLCWILCTSLKQEMQKGG	DLALTCQ ----
19.7	RKNETLFHSCSAPMVCWTVCSCLKQPKVRY	DLQSITQ ----
19.2	MENTILFSMCRVPVVCWMVCSGLKQQMERGN	NLTQSCP ----
11.1	QKNDILYKACQVPGICWVVCVSWLQGQMERGK	VVLETPT ----
Nalp2/19.4	RSNAALFQLGSAPAVCWIVCTTLKLQMEKGE	DPVPTCL ----
19.8	MNNRELLDQCQVPAVGSLICVALQLQDVVGE	SVAPFNQ ----
11.4	KENETLFALCFVPFVCWIVCTVLRQQLELGR	DLSRTSK ----
19.6	HEDEILVGLCRVAILCWITCTVLKRQMDKGR	DFQLCCQ ----
X	XENEDLDIMSSLPIVSWMICNVLQSQGDGDR	TLLRSLQ ----
11.3	EGHHQIAAACFLPSYCWLVCATLHFLHAPTP	AGQ ----
CIITA	RDRPLLLSHSHSPTLCRAVCQLSEALLELGE	DAKLPS ----
16.1	QTNGRLRSLCAVPALCQVACLCLHHLLPDHA	PGQSVALLP --
16.2	QADRALYLMCTVPAFCRLTGMAIGHLWRSRT	GPQDAELWPPR
Nod2	QETSALHGLCHLPVFSWMVSKCHQELLLQEG	GSPK ----
Nod1	EANPNLCSLCSVPLFCWIIIFRCFQHFRAAFE	GSPQLPDC -TM
Ipaf	QKSRCLRNLMKTPLFVVITCAIQMGSESEFHS	HTQTTLF ----
NAIP	GKNQSLQKIQTPLFVAAICAHWFQYPFDPS	FDDVAVF ----

MOTIF VII

MOTIF VIII²

1.1	TSTAVYVFFLSSLLQ	PRGGSQEH - - - - -	GLCA -	HLWGLC
19.3	TTTAVYMLYLLSLMQ	PKPGAPRL - - - - -	QPPP -	NQRGLC
19.1	NTTYLYASFLTTFVK	AGSQSFPPK - - - - -	VNRA -	RLKSLC
12	HLLKMNASFLTNTVFK	AGSQSFPPK - - - - -	VNRA -	RLKSLC
DEFCAP	TTTTLCLHYLAQALQ	AQPLGP - - - - -		QLRDLC
11.2	TTTALFTCYISSLFT	PVDGGSPSL - - - - -	PNQA -	QLRRLC
19.5	STTSVYSSFVFNLF	PEGAEGPTP - - - - -	QTQH -	QLKALC
19.7	TTTSLYAYFFSNLFS	TAEVDLADD - - - - -	SWPG -	QWRALC
19.2	NATSVFVRYISSLFP	TRAENFSRK - - - - -	IHQA -	QLEGLC
11.1	NSTDIFMAYVSTFLP	PDDDGCCSE - - - - -	LSRHR	VLRSLC
Nalp2/19.4	TRTGLFLRFLCSRFP	QGAQLRG - - - - -		ALRTLS
19.8	TLTGLHAAFVHFQLT	PRGVVRRCLN - - - - -	LEERV	VLRKRC
11.4	TTTSVYLLFITSVLS	SAPVADGPR - - - - -	LQG -	DLRNLC
19.6	TPTDLHAHFLADALT	SEAGLTANQY - - - - -	HLG -	LLKRRC
X	TMTDVYLFYFSKCLK	TLTGISVWE - - - - -	GQS	CLWGLC
11.3	TLTSIYTSFLRLNFS	GETLDSTDPSNL - - - - -	SLMAY	AARTMG
CIITA	TLTGLYVGLLGRAAL	DSPPG - - - - -		ALAEAL
16.1	NMTQLYMQMVLALSP	PGHLPTS - - - - -		SLLDLG
16.2	TLCELYSWYFRMALS	GEGQEK GKAS - - - - -	PRIEQVAHGGRK	MVGTLG
Nod2	TTTDMYLLILQHFL	HATPPDSASQ - - - - -	GLGPSLLRGRLP	TLLHLG
Nod1	TLTDVFLLVTEVHLN	RMQPSSLVQRNTRSPVETLHAGR		TLCSLG
Ipaf	- - - - - HTFYDL	LIQKNKHKHKG - - - - -	VAASDFIR	SLDHCG
NAIP	- - - - - KSYMER	LSLRNK - - - - -	ATAEILKA	TVSSCG

MOTIF VIII²

1.1	SLAADGIWNQKILFEESDLRNHGLQKA - DVSAFLRMNLFQK	EVD - -
19.3	SLAADGLWNQKILFEEQDLRKHGLDGE - DVSAFLNMNIFQK	DIN - -
19.1	ALAAEGIWYTFVFSHGLRRNGLSES - EGVMMWVGMRLQLR	R - - -
12	ALAAEGIWTHAFVF - - - DLWRNGLSES - EGLMWVGMKLLQR	X - - -
DEFCAP	SLAAEGIWQKKTFLSPDDLRRKHGLDGA - IISTFLKMGILQE	HP - - -
11.2	QVAAKGIWMTYVIFYRENLRRLGLTQS - DVSSFMDSNIIQK	DAE - -
19.5	SLAAEGMWTDTFEFCEDDLRRNGVVD - DIPALLGTKILLK	YGE - -
19.7	SLAIEGLWSMNFTFNKEDTEIEGLEVP - FIDSLYEFNILQK	IND - -
19.2	HLAADSMWHRKWVLGKEDLEEAKLDQT - GVTAFLGMSILRR	IAG - -
11.1	SLAAEGIQHQRFLEEEALRKHNLDGP - RLAAFLSSNDYQL	GLA - -
Nalp2/19.4	LLAAQGLWAQTSVLHREDLERLGVQES - DLRLFLDGDILRQ	DRV - -
19.8	RMAVEGVWNRKSVFDGDDLMLVQGLGES - ELRALFHMNILLP	DSH - -
11.4	RLAREGVLGRRQAFAEKELEQLELRGSKVQTLFLSKKELPG	VLE - -
19.6	LLAAGGLFLSTLNFSGEDLRCVGFTEA - DVSVLQAAANILLP	SNT - -
X	RLAAEGLQNHQVLFVAVSDLRRHGIGVCDTNCTFLSRFLKKA	EG - - -
11.3	KLAYEGVSSRKTYFSEEDVCGCLEAGIRTEEEFQLLHIFRR	DALRF
CIITA	KLAWELGRRHQSTLQEDQFPSADVRTWAMAK - - - - - GLVQH	PPR - -
16.1	EVALRGLETGKVIIFYAKDIAPPLIAFGATHSLLTSFCVCTG	PG - - -
16.2	RLAFHGLLKKKYVFYEQDMKAFGVDLALLQGAPCSCFLQRE	ETL - -
Nod2	RLALWGLGMCCYVFSQQQLQAAQVSPDDISLGFLVRAKGVV	PG - - -
Nod1	QVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELG	PGG - -
Ipaf	DLALEGVFVSHKFDVSSVNEVDVLLTTGLLC - - - - -	- - - - -
NAIP	ELALKGFFSCCFEFNDDDLAEAGVDEDEDLTMCL - - - - -	- - - - -

Rec'd PCT/PTO 21 OCT 2004

MOTIF IX³

* * * * *

1.1	-----CEK	FYSFIHMTFQEFFAAMYLLLE	EEKEGRTNV ---
19.3	-----CER	YYSFIHLSFQEFFAAMYIILD	EGEGGAG -----
19.1	-----GD	CFAFMHLCIQEFCAAMFYLLK	RPKDDPN -----
12	-----GE	CFTFIHVCIQEFCAATMFYLLK	RPKDDPN -----
DEFCAP	-----IPL	SYSFIHLCFQEFFAAMSIVLE	DEKGRGKHS ---
11.2	-----YEN	CYVFTHLHVQEFFAAMFYMLK	GSWEAGNP ----
19.5	-----RES	SYVFLHVCIQEFCAALFYLLK	GSWEAGNP ----
19.7	-----CGG	CTTFTHLVSFQEFFAAMSFVLE	EPREFPP -H---
19.2	-----EED	HYVFTLVTFQEFFAALFYVLC	FPQRLKN -----
11.1	-----IKK	FYSFRHISFQDFFHAMSIVLK	EDQSRLG -----
Nalp2/19.4	-----SKG	CYSFIHLSFQQFLTALFYTLE	KEEEEDRD ----
19.8	-----CEE	YYTFFHLSLQDFCAALYYVLE	GLEIEPALC ---
11.4	-----TEV	TYQFIDQSQEFFLAALSYLE	DGGVPRP -----
19.6	-----HKD	RYKFIHLNVQEFCTAIAFLMA	VPNYLIP -----
X	-----AVS	VYTFLHFSFQEFLLTAVFHALK	NDNSWMF -----
11.3	FLAPC VEPGRAG	TFVFTVPAMQEYLAALYIVLG	LRKTTLQ -----
CIITA	-----AAES	ELAFPSFLLQCFLLGALWLAES	GEIKDKE -----
16.1	-----HQOT	GYAFTHLSLQEFLLAALHLMAS	PKVKNKDT -----
16.2	-----ASSV	AYCFTHLSLQEFVAAAYYYGA	SRRAIFDLFTES
Nod2	-----STA	PLEFLHITFQCFFAAFYLALS	ADVPPALLRHLF
Nod1	-----DQQ	SYEFFHLTLQAFFTAFFLVLD	DRVGTQELLRFF
Ipaf	---KYTAQRFKP	KYKFFHKSFQEYTAGRRLSSL	L
NAIP	-MSKFTAQRLRP	FYRFLSPAQEFLLAGMRLIEL	L

1.1	-----	PGSRLKLP SRDVTV LLENY GKF EK -GYLI FVV
19.3	-----	PDQDVTRLLTEYAFSER -SFLALTS
19.1	-----P-----	AIGSITQLVRASVVQPQ -TLLTQVG
12	-----P-----	TIGSITQLVRASVAQPQ -THSTQVG
DEFCAP	-----N-----	CIIDLEKTLEAYGIHG --LFGASTT
11.2	-----S-----	CQPFEDLKSLQSTSYKD --PHLTQMK
19.5	-----	AVRCVQELLVANFEKARRAHWIFLG
19.7	-----S-----	TKPQEMKMLLQHVLLDKEAYWTPVV
19.2	-----	FHVLSHVNIQRLIASPRGSKSYLSHMG
11.1	-----K-----	ESRREVQRLLEVKEQEGN -DEMTLTM
Nalp2/19.4	-----	GHTWDIGDVQKLLSGVERLRN -PDLIQAG
19.8	-----P-----	LYVEKTKRSMELKQAGFHIHSLWMK
11.4	-----	AAGGVGTLLRGDAQPHS --HLVLTT
19.6	-----S-----	GSREYKEKREQYSDFNQVF
X	-----	FYQAEKMWQEMFQQYG -KGFSSSLMI
11.3	---	KVGKEVAELVGRVGEDVSLVLGIMAKLLPLRALPLLFNLIKVV
CIITA	-----	LPQYLALTPRKKRPYDNWLEGVP
16.1	-----	LTQYVTLHSRWVQRTKARLGLSDHLP
16.2	-----G-----	VSWPRLGFLTHFRSAAQAMQAEDGRLDVFL
Nod2	NCGRPGNSPMARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITA	
Nod1	QEWMPAGAATTSCYPFPLPFQCLQSGPAREDLFKNKDHQFTN	

Ipaf (SEQ ID NO:183)
NAIP (SEQ ID NO:184)

MOTIF X

MOTIF X

1.1	RFLFGLVN	QERT-----	SYLEKKLSCMISQQIRL	ELLKWIE
19.3	RFLFGLLN	EETR-----	SHLEKSLCWKVSPHIKM	DLLQWIQ
19.1	IFMFGIST	EEIV-----	SMLETSFGFPPLSKDLKQ	EITQCLE
12	VFVFGIST	EEII-----	SLETSFGFPPLKDLKK	EITQCLK
DEFCAP	RFLLGLLS	DEGE-----	REMENIFHCRLSQ--GR	NLMQWVP
11.2	CFLFGLLN	EDRV-----	KQLERTFNCKMSLKIKS	KLLQCME
19.5	CFLTGLLN	KKEQ-----	EKLDAFFGFQLSQEIKQ	QIHQCLK
19.7	LFFFGLLN	KNIA-----	RELEDTLHCKISPRVME	ELLKWGE
19.2	LFLFGFLN	EACA-----	SAVEQSFQCKVSFGNKR	KLLKVIP
11.1	QFLLDISK	KDSF-----	SNLELKFCFRISPCLAQ	DLKHFKE
Nalp2/19.4	YYSFGLAN	EKRA-----	KELEATFGCRMSPDIKQ	ELLRCDI
19.8	RFLFGLVS	EDVR-----	RPLEVLLGCPVPLGVKQ	KLLHWVS
11.4	RFLFGLLS	AERM-----	RDIERHFGCMVSERVKQ	EALRWVQ
19.6	TFIFGLLN	ANRR-----	KILETSFGYQLPMVDSF	KWYSVGY
X	XFLFGLLH	KGKG-----	KAVETTFGRKVSPGLQE	ELLKWTE
11.3	PRVFGRMV	GKSR-----	RAVLAQLGCPIKNLDAL	ENAAQAIK
CIITA	RFLAGLIF	QPPA-----	RCLGALLGPSAAASVDR	KQKVLAR
16.1	TFLAGLAS	CTCR-----	-PFLSHLAQGNEDCVGA	KQAAVVQ
16.2	RFLSGLLS	PRVN-----A	LLAGSLLAQGEHQAYRT	QVAELLQ
Nod2	AFLAGLLS	REHWG-----	LLAECQTSEKALLRRQA	CARWCLA
Nod1	LFLCGLLS	KAKQKLL---R	HLVPAAALRRKRKALWA	HLFSSLR

1.1	VKAK-----	AKKLHDQPS
19.3	SKAQ-----	SDGSTLQQG
19.1	SLSQ-----	CEADREAIA
12	SLSQ-----	XEADREVIG
DEFCAP	SLQ-----	LLLQPH
11.2	VLGN-----	SDYSPSQLG
19.5	SLGE-----	RGNPQGQVD
19.7	ELGK-----	AESASLQFH
19.2	LLHK-----	CDPPSPGSG
11.1	QMES-----	MKHNRTWDL
Nalp2/19.4	SCKG-----	GHSTVTD
19.8	LLGQ-----	QPNATTPGD
11.4	GQGQGCPGVAPEVTEGAKGLEDTEEPEEEEEGEEPNY	
19.6	MKHL-----	RDPEKLTH
X	REIK-----	DKSSRLQIE
11.3	KKLG-----	KLGRQVLPPE
CIITA	YLKR-----	LQPGTLRARQ
16.1	VLKK-----	LATRKLTPGPK
16.2	GCLR-----	PDAAVCAR
Nod2	RSLR-----	KHFHSIPPAAPGEAKSVHAMPG
Nod1	GYLKSLPR-----	VQVESFNQVQAMPT

MOTIF XI

1.1	QLELFYCLYEMQEEDFVQRAMDYFPKIEIN -	-L--STR
19.3	SLEFFSCLYEIQEEEFIQQALSHFQVIVVSN	-I--ASK
19.1	FQELFIGLFETQEKEFVTKVMNFFEEVFIY -	-I--GNI
12	FQELFHDLFATQEKEFVTEVINFFEEVFIC -	-T--GNI
DEFCAP	SLES LHCLYETRNTFLTQVMAHFEE MGMC -	-V--ETD
11.2	FLELFHCLYETQDKAFISQAMRCFPKVAIN -	-I--CEK
19.5	SLAIFYCLFEMQDPAFVKQAVNLLQEANFH -	-I--IDN
19.7	ILRLFHCLHESQEEDFTKKMLGRIFEVDLN -	-I--LED
19.2	VPQLFYCLHEIREEAFVSQALNDYHKVVLR -	-I--GNN
11.1	EFSLYEAKIKNLVKGIQMNVSFKIKHSNEK	-K--SQS
Nalp2/19.4	LQELLGCLYESQEEELVKEVMAQFKEISLH -	----LNA
19.8	TLDAFHCLFETQDKEFVRLALNSFQEVWLP -	-I--NQN
11.4	PLELLYCLYETQEDAFVRQALCRFPPELALQR	-V-RFCR
19.6	HMP LFYCLYENREEEFVKTIVDALMEVTVYL	-Q---SD
X	PVDLFHCLYEIQEEYAKRIIDDLQSIILLQ	PT--YTK
11.3	LLDHLFFHYEFQNRFSAEVLSSLRQLNLAG	-V-RMTP
CIITA	LLELLHCAHEAEEAGIWQHVQELPGRLSFL	G-TRLTP
16.1	VVELCHCVDETQEP ELASLTAQSLPYQLPFH	N-FPLTC
16.2	AINVLHCLHELQHTELARSVEEAMESGALAR	LTGPAHR
Nod2	FIWLIRSLYEMQEERLARKAARGLNVGHLKL	TFC SVGP
Nod1	FIWMLRCIYETQSQKVGQLAARGICANYLKL	TYCNACS

MOTIF XII

1.1	MDH MVSSFCIENCHRVESLSLGF	(SEQ ID NO:162)
19.3	MEH MVSSFCLKRCRSAQVLHLYG	(SEQ ID NO:163)
19.1	EHLV IASFCLKHCQH LTTLRMCV	(SEQ ID NO:164)
12	EHLV VSSFCRKHCQN LTTLRMCV	(SEQ ID NO:165)
DEFCAP	MELLVCTFCIKFSRHVKKLQ LIE	(SEQ ID NO:166)
11.2	IHLV VSSFCLKHCRCLRTIRLSV	(SEQ ID NO:167)
19.5	VDLVVSAYCLKYCSSLRKLCFSV	(SEQ ID NO:168)
19.7	EELQASSFCLKHCKRLNKLRLSV	(SEQ ID NO:169)
19.2	KEVQVSAFCLKRCQYLHEVELT -	(SEQ ID NO:170)
11.1	QNLFSVKSSLSHGPKEEQKCPSV	(SEQ ID NO:171)
Nalp2/19.4	VDVVPSSFCVKHCRNLQKMSLQV	(SEQ ID NO:172)
19.8	LDLIASSFCLQHCPYLRLKIRVDV	(SEQ ID NO:173)
11.4	MDVAVLSYCVRCCPAGQALRLIS	(SEQ ID NO:174)
19.6	KDM MVSLYCLDYCCHLRTLKLSV	(SEQ ID NO:175)
X	MDILVMSFCVKSSHSHLSVSLKC	(SEQ ID NO:176)
11.3	VKCTVVAAVLGSGRHALDEVNLA	(SEQ ID NO:177)
CIITA	PDAHVLGKALEAAGQDFSLDLRS	(SEQ ID NO:178)
16.1	TDLATLTNILEHREAPIHLDFDG	(SEQ ID NO:179)
16.2	AALAYLLQVSDACAQEANLSLSL	(SEQ ID NO:180)
Nod2	TECAALAFVLQH LRRPVALQLDY	(SEQ ID NO:181)
Nod1	ADCSALSFVLHHFPKRLALDLN	(SEQ ID NO:182)

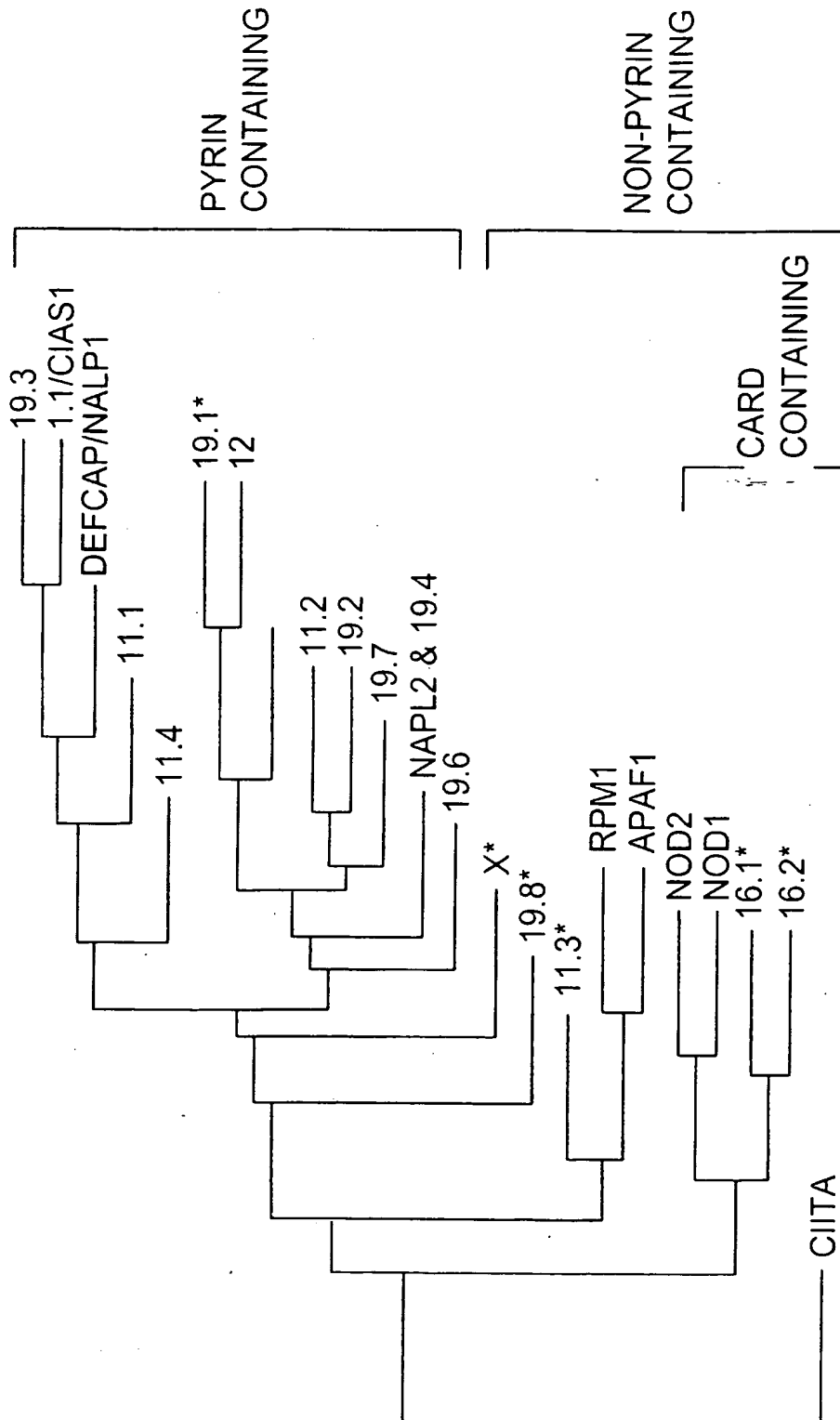


FIG.4

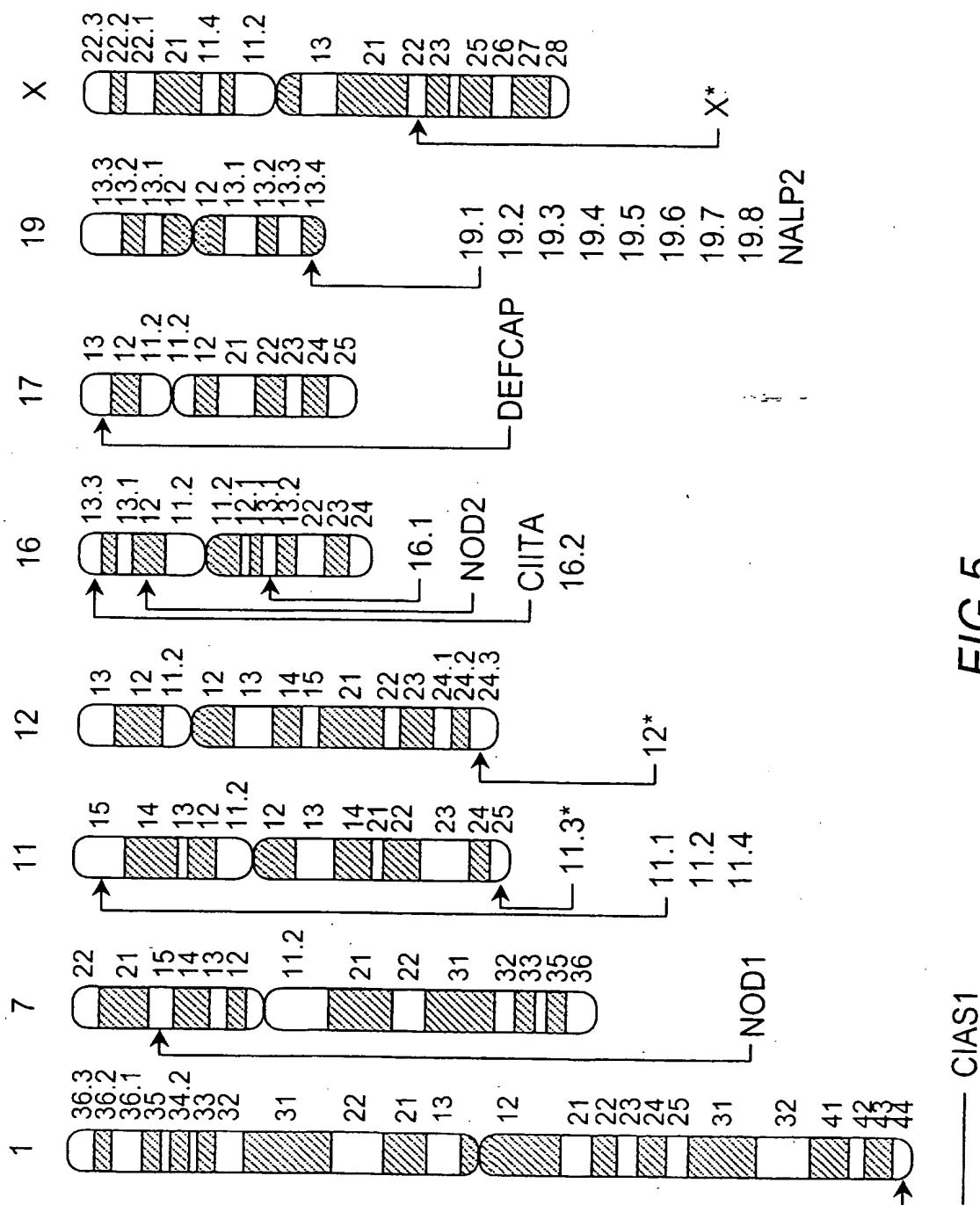


FIG.5

Rec'd PCT/PTO 21 OCT 2004

1 ATTTGGTGAGTGGGGCAGGGCAGGAGGGAACTGAAGAGTGAGAAAGCATT
51 TTTTTCAGCAAAAGGTCTTTTCTCCCTTGCTCACTCCTCCAACCACTGGCTC
101 AGCCTCTCCGCCCCGCTGCCTGTGAATGATGCAATGGAAGGTGTGCTGGGG
151 TCGCCCTGTGTCCCGTGCATAGGAGCATCTCAGCCTCCAGGTCTCTCCT
201 TTGGGGCTTACGGCACCCCCATGTACGAACCGCAGGCAGGGACGGCCTC
251 TGTCGCCTGTCCACCTACTTGAAGAACTCGAGGCTGTGGAAGTGAAGAA
301 GTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAAGGCAAGATCC
351 CCTGGGGAAGCATGGAGAAGGCCGGTCCCCTGGAAATGGCCCAGCTGCTC
401 ATCACCCACTTCGGGCCAGAGGAGGCCTGGAGGTTGGCTCTCAGCACCTT
451 TGAGCGGATAAACAGGAAGGACCTGTGGGAGAGAGGACAGAGAGAGGACC
501 TGGTGAGGGATACCCCACTGGTGGCCCCGTCTCACTTGGGAACCACTCA
551 ACATGCCTTCTGGAAGTCTCTTGTCACTCCAAGAAAAGATCCCCAGGA
601 AACCTACAGGGACTATGTCCGCAGGAAATTCGGGCTCATGGAAGACCGCA
651 ATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC
701 CTGCTGGTGAAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCT
751 GGACACAGGCCGGGGACACGCGAGGACCGTGGGACACCAAGGCTAGCCCCA
801 TCAAGATAGAGACCTCTTTGAGCCAGACGAGGAGCGCCCCGAGCCACCG
851 CGCACCGTGGTTCATGCAAGGCGCGGCAGGGATAGGCAAGTCCATGCTGGC
901 ACACAAGGTGATGCTGGACTGGGCGGACGGGAAGCTCTTCCAAGGCAGAT
951 TTGATTATCTCTTCTACATCAACTGCAGGGAGATGAACCAGAGTGCCACG
1001 GAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGCCCAGCGC
1051 GCCTCTCCAGGAGCTCATCCGAGTTCCTCCGAGCGCCTCCTTTTCATCATCG
1101 ACGGCTTCGATGAGCTCAAGCCTTCTTTCCACGATCCTCAGGGACCCTGG
1151 TGCCTCTGCTGGGAGGAGAAACGGCCCCACGGAGCTGCTTCTTAACAGCTT
1201 AATTCCGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACCACACGGC
1251 CCACGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGCACCCCAAGCATGTG
1301 GAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCTACAAGTA
1351 TTTCCACAATGCAGAGCAGGCGGGGCCAAGTCTTCAATTACGTGAGGGACA
1401 ACGAGCCTCTCTTACCATGTGCTTTCGTCCTCCCTGGTGTGCTGGGTGGTG
1451 TGTACCTGCCTCCAGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGAC
1501 GTCCAGGACCACCACTGCAGTGTACATGCTCTACCTGCTGAGTCTGATGC
1551 AACCCAAGCCGGGGGCCCCGCGCCTCCAGCCCCACCCAACCAGAGAGGG
1601 TTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCCTATTTGA
1651 GGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCT
1701 TCCTCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGTACTAC
1751 AGCTTCATCCACTTGAGTTTCCAGGAATTCTTTGCAGCTATGTACTATAT
1801 CCTGGACGAGGGGGAGGGCGGGGCAGGCCAGACCAGGACGTGACCAGGC
1851 TGTTGACCGAGTACGCGTTTTTCTGAAAGGAGCTTCTTGGCACTCACCAGC
1901 CGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAA
1951 GAGTCTCTGCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGCAGT
2001 GGATCCAAAGCAAAGCTCAGAGCGACGGCTCCACCCTGCAGCAGGGCTCC
2051 TTGGAGTTCTTCAGCTGCTTGTACGAGATCCAGGAGGAGGAGTTTATCCA
2101 GCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTGCCTCCA
2151 AGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCGCC
2201 CAGGTGCTGCACTTGTATGGCGCCACCTACAGCGCGGACGGGGAAGACCG
2251 CGCGAGGTGCTCCGCAGGAGCGCACACGCTGTTGGTGCAGCTCAGACCAG
2301 AGAGGACCGTTCTGCTGGACGCCTACAGTGAACATCTGGCAGCGGCCCTG
2351 TGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAAATGCCCTGGG
2401 CAGCCGGGGGGTGAAGCTGCTGTGTCAAGGACTCAGACACCCCAACTGCA
2451 AACTTCAGAACCTGAGGCTGAAGAGGTGCCGCATCTCCAGCTCAGCCTGC
2501 GAGGACCTCTCTGCAGCTCTCATAGCCAATAAGAATTTGACAAGGATGGA

FIG. 6A

13/68

2551 TCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCTTTGCGAGG
 2601 GCCTGCGGCATCCCCAGTGCAGGCTGCAGATGATTGAGTTGAGGAAGTGT
 2651 CAGCTGGAGTCCGGGGCTTGTGAGGAGATGGCTTCTGTGCTCGGCACCAA
 2701 CCCACATCTGGTTGAGTTGGACCTGACAGGAAATGCACTGGAGGATTTGG
 2751 GCCTGAGGTTACTATGCCAGGGACTGAGGCACCCAGTCTGCAGACTACGG
 2801 ACTTTGTGGCTGAAGATCTGCCGCCTCACTGCTGCTGCCTGTGACGAGCT
 2851 GGCCTCAACTCTCAGTGTGAACCAGAGCCTGAGAGAGCTGGACCTGAGCC
 2901 TGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCTCAGG
 2951 CATCCACGTGCAAGCTCCAGACCCTGCGGTTGGGCATCTGCCGGCTGGG
 3001 CTCTGCCGCCTGTGAGGGTCTTTCTGTGGTGTCTCCAGGCCAACCACAACC
 3051 TCCGGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCCTGTGG
 3101 TTGCTGGCTGAGGGGCTGCAACATCCCGCCTGCAGACTCCAGAACTGTG
 3151 GCTGGATAGCTGTGGCCTCACAGCCAAGGCTTGTGAGAATCTTTACTTCA
 3201 CCCTGGGATCAACCAGACCTTGACCGACCTTTACCTGACCAACAACGCC
 3251 CTAGGGGACACAGGTGTCCGACTGCTTTGCAAGCGGCTGAGCCATCCTGG
 3301 CTGCAAACTCCGAGTCCTCTGTTATTTGGGATGGACCTGAATAAAATGA
 3351 CCCACAGTAGGTTGGCAGCGCTTCGAGTAACAAAACCTATTTGGACATT
 3401 GGCTGCTGAATGGTCTATCTGCTGGCTCTCCCCTGAGATCTGGACAGAG
 3451 GAAGATGGGAGGGTGCTCATCAACCCCCCAGCATAATGATCAGCCTCCTT
 3501 CCTAGAGACAGACTCATGCAGATTGAGATCAAAAGTCCCTCTGCTTGGGA
 3551 TCAAATTAATGTTTGACAGAGCTGGCCAGGCGTGGTGGCTCATGTATGTA
 3601 ATCCTAGCACTTCGAGAGGCCGAGGCAGGTGGATCACGAGGTCAGGAGTT
 3651 TGAGATTAGCCTGGCCAAGATGGTGAAACCCTGTCTCTACTAAAAATAAA
 3701 AAAAAATTAGCCAGGAAAAA (SEQ ID NO:1)

FIG. 6B

1 MLRTAGRDGLCRLSTYLEELEAVELEKKFKLYLGTATELGEGKIPWGSMEK
 51 AGPLEMAQLLIITHFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPP
 101 GGPSSLGNQSTCLLEVSLVTPRKDPQETRYRDYVRRKFRLMEDRNARLGEC
 151 VNLSHRYTRLLLKVKEHSNPMQVQQQLDGTGRGHARTVGHQASPIKIETLF
 201 EPDEERPEPPRTVVMQGAAGIGKSM LAHKVMLDWADGKLFQGRFDYLFYI
 251 NCREMNQSATECSMQDLIFSCWPEPSAPLQELIRVPERLLFIIDGFDELK
 301 PSFHDPQGPWCLCWECKRPTTELLLSLIRKKLLPELSLLITRPTALEKL
 351 HRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNYVRDNEPLFTM
 401 CFVPLVCWVCTCLQQOLEGGGLLRQTSRTTAVYMLYLLSLMQPKPGAP
 451 RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIF
 501 QKDINCERYYSFIHLSFQEFFAAMYIILDEGEGGAGPDQDVTRLLTEYAF
 551 SERSFLALTSRFLFGLLNEETRSHLEKSLCWKVSPIHKMDLLQWISKAQ
 601 SDGSTLQQGSLEFFSCLYEIQEEFIQQALSHFQVIVVSNIAASKMEHMVS
 651 SFCLKRCRSAQVLHLYGATYSADGEDRARC SAGAHTLLVQLRPERTVLLD
 701 AYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRHPNCKLQNLRL
 751 KRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHPQC
 801 RLQMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQ
 851 GLRHPVCRLRTLWLKICRLTAAACDELASTLSVNQSLRELDLSLNELGDL
 901 GVLLLCGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRELDLS
 951 FNDLGDWGLWLLAEGLOHPACRLQKLWLDSCGLTAKACENLYFTLGINQT
 1001 LTDLYLTNNALGDTGVRLLCRLSHPGCKLRVLWLFGMDLNKMTHSRLAA
 1051 LRVTKPYLDIGC (SEQ ID NO:2)

FIG. 6C

1 ATTGGTGAGTGGGGCAGGGCAGGAGGGAAGTGAAGAGTGAGAAAGCATT
51 TTTCAGCAAAAAGGTCTTTTCCCTCCCTTGCTCACTCCTCCAACCACTGGCTC
101 AGCCTCTCCGCCCCGCTGCCTGTGAATGATGCAATGGAAGGTGTGCTGGGG
151 TCGCCCTGTGTCCCGTGCATAGGAGCATCTCAGCCTCCAGGTCCTCTCCT
201 TTGGGGCTTACGGCACCCCCATGCTACGAACCGCAGGCAGGGACGGCCTC
251 TGTCGCCTGTCCACCTACTTGAAGAAGTTCGAGGCTGTGGAAGTGAAGAA
301 GTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAAGGCAAGATCC
351 CCTGGGGAAGCATGGAGAAGGCCGGTCCCCTGGAAATGGCCCAGCTGCTC
401 ATCACCCACTTCGGGCCAGAGGAGGCCTGGAGGTTGGCTCTCAGCACCTT
451 TGAGCGGATAAACAGGAAGGACCTGTGGGAGAGAGGACAGAGAGAGGACC
501 TGGTGAGGGATAACCCACCTGGTGGCCCGTCCCTCACTTGGGAACCACTCA
551 ACATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAAGATCCCCAGGA
601 AACCTACAGGGACTATGTCCGCAGGAAATTCGGGCTCATGGAAGACCGCA
651 ATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCCGGCTC
701 CTGCTGGTGAAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCT
751 GGACACAGGCCGGGGACACGCGAGGACCGTGGGACACCAGGCTAGCCCCA
801 TCAAGATAGAGACCCCTCTTTGAGCCAGACGAGGAGCGCCCCGAGCCACCG
851 CGCACCGTGGTTCATGCAAGGCGCGGCAGGGATAGGCAAGTCCATGCTGGC
901 ACACAAGGTGATGCTGGACTGGGCGGACGGGAAGCTCTTCCAAGGCAGAT
951 TTGATTATCTCTTCTACATCAACTGCAGGGAGATGAACCAGAGTGCCACG
1001 GAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGCCCAGCGC
1051 GCCTCTCCAGGAGCTCATCCGAGTTCCTGAGCGCCTCCTTTTCATCATCG
1101 ACGGCTTCGATGAGCTCAAGCCTTCTTTCCACGATCCTCAGGGACCCCTGG
1151 TGCTCTGCTGGGAGGAGAAACGGGCCACGGAGCTGCTTCTTAACAGCTT
1201 AATTGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACCACACGGC
1251 CCACGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGCACCCAGGCATGTG
1301 GAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCTACAAGTA
1351 TTTCCACAATGCAGAGCAGGCGGGCCAAGTCTTCAATTACGTGAGGGACA
1401 ACGAGCCTCTCTTCACCATGTGCTTCGTCCCCCTGGTGTGCTGGGTGGTG
1451 TGTACCTGCCTCCAGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGAC
1501 GTCCAGGACCACCACTGCAGTGTACATGCTCTACCTGCTGAGTCTGATGC
1551 AACCCAAGCCGGGGGCCCCGCGCCTCCAGCCCCACCCAACCAGAGAGGG
1601 TTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCCTATTTGA
1651 GGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCT
1701 TCCTCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGTACTAC
1751 AGCTTCATCCACTTGAGTTTCCAGGAATTCTTTGCAGCTATGTACTATAT
1801 CCTGGACGAGGGGGAGGGCGGGGCAGGCCAGACCAGGACGTGACCAGGC
1851 TGTTGACCGAGTACGCGTTTTCTGAAAGGAGCTTCCTGGCACTCACCAGC
1901 CGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAA
1951 GAGTCTCTGCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGCAGT
2001 GGATCCAAAGCAAAGCTCAGAGCGACGGCTCCACCCTGCAGCAGGGCTCC
2051 TTGGAGTTCTTCAGCTGCTTGTACGAGATCCAGGAGGAGGAGTTTATCCA
2101 GCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTGCCTCCA
2151 AGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCGCC
2201 CAGGTGCTGCACTTGTATGGCGCCACCTACAGCGCGGACGGGGAAGACCG
2251 CGCGAGGTGCTCCGCAGGAGCGCACACGCTGTTGGTGCAGCTCAGACCAG
2301 AGAGGACCGTTCTGCTGGACGCCTACAGTGAACATCTGGCAGCGGCCCTG
2351 TGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAAATGCCCTGGG
2401 CAGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCAACTGCA
2451 AACTTCAGAACCTGAGGCTGAAGAGGTGCCGCATCTCCAGCTCAGCCTGC
2501 GAGGACCTCTCTGCAGCTCTCATAGCCAATAAGAATTTGACAAGGATGGA

2551 TCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCTTTGCGAGG
2601 GCCTGCGGCATCCCCAGTGCAGGCTGCAGATGATTCAGTTGAGGAAGTGT
2651 CAGCTGGAGTCCGGGGCTTGTCTAGGAGATGGCTTCTGTGCTCGGCACCAA
2701 CCCACATCTGGTTGAGTTGGACCTGACAGGAAATGCACTGGAGGATTTGG
2751 GCCTGAGGTTACTATGCCAGGGACTGAGGCACCCAGTCTGCAGACTACGG
2801 ACTTTGTGGCTGAAGATCTGCCGCCTCACTGCTGCTGCCTGTGACGAGCT
2851 GGCTCAACTCTCAGTGTGAACCAGAGCCTGAGAGAGCTGGACCTGAGCC
2901 TGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCTCAGG
2951 CATCCACGTGCAAGCTCCAGACCCTGCGGTTGGGCATCTGCCGGCTGGG
3001 CTCTGCCGCCTGTGAGGGTCTTTCTGTGGTGCTCCAGGCCAACCACAACC
3051 TCCGGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCCTGTGG
3101 TTGCTGGCTGAGGGGCTGCAACATCCCGCCTGCAGACTCCAGAACTGTG
3151 GTGGTTATTTGGGATGGACCTGAATAAAATGACCCACAGTAGGTTGGCAG
3201 CGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGAATGGTCTTA
3251 TCTGCTGGCTCTCCCCTGAGATCTGGACAGAGGAAGATGGGAGGGTGCTC
3301 ATCAACCCCCCAGCATAATGATCAGCCTCCTTCCTAGAGACAGACTCATG
3351 CAGATTGAGATCAAAAGTCCCTCTGCTTGGGATCAAATTAATGTTTGACA
3401 GAGCTGGCCAGGCGTGGTGGCTCATGTATGTAATCCTAGCACTTCGAGAG
3451 GCCGAGGCAGGTGGATCACGAGGTGAGGAGTTTGAGATTAGCCTGGCCAA
3501 GATGGTGAAACCCTGTCTCTACTAAAAATAAAAAAAAAATTAGCCAGGAAA
3551 AAAAAAAAAAAAAA (SEQ ID NO:3)

FIG. 6E

1 MLRTAGRDGLCRLSTYLEELEAVELEKKFKLYLGTATELGEGKIPWGSMEK
51 AGPLEMAQLLI THFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPP
101 GGPSSLGNQSTCLLEVSLVTPRKDPQETYRDYVRRKFRLMEDRNARLGEC
151 VNLSHRYTRLLLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLF
201 EPDEERPEPPRTVVMQGAAGIGKSMLAHKVMLDWADGKLFQGRFDYLFYI
251 NCREMNQSATECSMQDLIFSCWPEPSAPLQELIRVPERLLFIIDGFDELK
301 PSFHDPPQGPWCLCWECKRPTTELLLSLIRKKLLPELSLLITRPTALEKL
351 HRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNYVRDNEPLFTM
401 CFVPLVCWVVTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
451 RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIF
501 QKDINCERYYSFIHLSFQEFFAAMYIILDEGEGGAGPDQDVTRLLTEYAF
551 SERSFLALTSRFLFGLLNEETRSHLEKSLCWKVSPHIMDQLLQWISKAQ
601 SDGSTLQQGSLEFFSCLYEIQEEEFIQQALSHFQVIVVSNIASKMEHMVS
651 SFCLKRCRSAQVLHLYGATYSADGEDRARCSAGAHTLLVQLRPERTVLLD
701 AYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCQGLRHPNCKLQNLRL
751 KRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHPQC
801 RLQMIQLRKQLESACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQ
851 GLRHPVCRLRTLWLKICRLTAAACDELASTLSVNQSLRELDLSLNEIGDL
901 GVLLLCGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRLRELDLS
951 FNDLGDWGLWLLAEGLOHPACRLQKLWWLFGMDLNKMTSRLAALRVTKP
1001 YLDIGC (SEQ ID NO:4)

FIG. 6F
16/68

1 ATTGGTGAGTGGGGCAGGGCAGGAGGGAACTGAAGAGTGAGAAAGCATT
51 TTTCAGCAAAAGGTCTTTCTCCCTTGCTCACTCCTCCAACCACTGGCTC
101 AGCCTCTCCGCCCCGCTGCCTGTGAATGATGCAATGGAAGGTGTGCTGGGG
151 TCGCCCTGTGTCCCGTGCATAGGAGCATCTCAGCCTCCAGGTCCTCTCCT
201 TTGGGGCTTACGGCACCCCATGCTACGAACCGCAGGCAGGGACGGCCTC
251 TGTCGCCTGTCCACCTACTTGGAAGAACTCGAGGCTGTGGAAGTGAAGAA
301 GTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAAGGCAAGATCC
351 CCTGGGGAAGCATGGAGAAGGCCGGTCCCCTGGAAATGGCCCAGCTGCTC
401 ATCACCCACTTCGGGCCAGAGGAGGCCTGGAGGTTGGCTCTCAGCACCTT
451 TGAGCGGATAAACAGGAAGGACCTGTGGGAGAGAGGACAGAGAGAGGACC
501 TGGTGAGGGATACCCACCTGGTGGCCCGTCCCTCACTTGGGAACCAAGTCA
551 ACATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAAGATCCCCAGGA
601 AACCTACAGGGACTATGTCCGCAGGAAATTCGGGCTCATGGAAGACCGCA
651 ATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC
701 CTGCTGGTGAAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCT
751 GGACACAGGCCCGGGACACGCGAGGACCGTGGGACACCAGGCTAGCCCCA
801 TCAAGATAGAGACCTCTTTGAGCCAGACGAGGAGCGCCCCGAGCCACCG
851 CGCACCGTGGTCATGCAAGGCGCGGCAGGGATAGGCAAGTCCATGCTGGC
901 ACACAAGGTGATGCTGGACTGGGCGGACGGGAAGCTCTTCCAAGGCAGAT
951 TTGATTATCTCTTCTACATCAACTGCAGGGAGATGAACCAGAGTGCCACG
1001 GAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGCCCAGCGC
1051 GCCTCTCCAGGAGCTCATCCGAGTTCCCGAGCGCCTCCTTTTCATCATCG
1101 ACGGCTTCGATGAGCTCAAGCCTTCTTTCCACGATCCTCAGGGACCCTGG
1151 TGCCTCTGCTGGGAGGAGAAACGGCCACGGAGCTGCTTCTTAACAGCTT
1201 AATTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACCAACGCGC
1251 CCACGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGCACCCAGGCATGTG
1301 GAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCTACAAGTA
1351 TTTCCACAATGCAGAGCAGGCGGGCCAAGTCTTCAATTACGTGAGGGACA
1401 ACGAGCCTCTCTTACCATGTGCTTCGTCCCCCTGGTGTGCTGGGTGGTG
1451 TGTACCTGCCTCCAGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGAC
1501 GTCCAGGACCACCACTGCAGTGTACATGCTCTACCTGCTGAGTCTGATGC
1551 AACCCAAGCCGGGGGCCCCGCGCCTCCAGCCCCACCCAACCAGAGAGGG
1601 TTGTGCTCCTTGCGCGCAGATGGGCTCTGGAATCAGAAAATCCTATTTGA
1651 GGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCT
1701 TCCTCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGTACTAC
1751 AGCTTCATCCACTTGAGTTTCCAGGAATTCTTTGCAGCTATGTACTATAT
1801 CCTGGACGAGGGGGAGGGCGGGCAGGCCAGACCAGGACGTGACCAGGC
1851 TGTTGACCGAGTACGCGTTTTCTGAAAGGAGCTTCCTGGCACTCACCAGC
1901 CGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAA
1951 GAGTCTCTGCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGCAGT
2001 GGATCCAAAGCAAAGCTCAGAGCGACGGCTCCACCCTGCAGCAGGGCTCC
2051 TTGGAGTTCTTCAGCTGCTTGTACGAGATCCAGGAGGAGGAGTTTATCCA
2101 GCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTGCCTCCA
2151 AGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCGCC
2201 CAGGTGCTGCACTTGTATGGCGCCACCTACAGCGCGGACGGGGAAGACCG
2251 CGCGAGGTGCTCCGCAGGAGCGCACACGCTGTTGGTGCAGCTCAGACCAG
2301 AGAGGACCGTTCTGCTGGACGCCTACAGTGAACATCTGGCAGCGGCCCTG
2351 TGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAAATGCCCTGGG
2401 CAGCCGGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCAACTGCA
2451 AACTTCAGAACCTGAGGCTGAAGAGGTGCCGCATCTCCAGCTCAGCCTGC
2501 GAGGACCTCTCTGCAGCTCTCATAGCCAATAAGAATTTGACAAGGATGGA

2551 TCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCTTTGCGAGG
2601 GCCTGCGGCATCCCCAGTGCAGGCTGCAGATGATTGAGGAAGTGT
2651 CAGCTGGAGTCCGGGGCTTGTGAGGAGATGGCTTCTGTGCTCGGCACCAA
2701 CCCACATCTGGTTGAGTTGGACCTGACAGGAAATGCACTGGAGGATTTGG
2751 GCCTGAGGTTACTATGCCAGGGACTGAGGCACCCAGTCTGCAGACTACGG
2801 ACTTTGTGGCTGTGGCTGGATAGCTGTGGCCTCACAGCCAAGGCTTGTGA
2851 GAATCTTTACTTCAACCCTGGGGATCAACCAGACCTTGACCGACCTTTACC
2901 TGACCAACAACGCCCTAGGGGACACAGGTGTCCGACTGCTTTGCAAGCGG
2951 CTGAGCCATCCTGGCTGCAAACTCCGAGTCCTCTGGTTATTTGGGATGGA
3001 CCTGAATAAAATGACCCACAGTAGGTTGGCAGCGCTTCGAGTAACAAAAC
3051 CTTATTTGGACATTGGCTGCTGAATGGTCCTATCTGCTGGCTCTCCCTG
3101 AGATCTGGACAGAGGAAGATGGGAGGGTGCTCATCACCCCCCAGCATAA
3151 TGATCAGCCTCCTTCCTAGAGACAGACTCATGCAGATTGAGATCAAAAGT
3201 CCCTCTGCTTGGGATCAAATTAATGTTTGACAGAGCTGGCCAGGCGTGGT
3251 GGCTCATGTATGTAATCCTAGCACTTCGAGAGGCCGAGGCAGGTGGATCA
3301 CGAGGTCAGGAGTTTGAGATTAGCCTGGCCAAGATGGTGAAACCTGTCT
3351 CTAATAAAATAAAAAAAAAATTAGCCAGGAAAAAAAAAAAAAAAAAAAA
(SEQ ID NO:5)

FIG. 6H

1 MLRTAGRDGLCRLSTYLEELEAVELEKKFKLYLGTATELGEGKIPWGSMEK
51 AGPLEMAQLLI THFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPP
101 GGPSSLGNQSTCLLEVSLVTPRKDPQETRYRDYVRRKFRLMEDRNARLGEC
151 VNLSHRYTRL LLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLF
201 EPDEERPEPPRTVVMQGAAGIGKSM LAHKVMLDWADGKLFQGRFDYLFYI
251 NCREMNQSATECSMQDLIFSCWPEPSAPLQELIRVPERLLFIIDGFDELK
301 PSFHDPQGPWCLCWECKRPTTELLLSLIRKKLLPELSLLITTRPTALEKL
351 HRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNYVRDNEPLFTM
401 CFVPLVCWVVCTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
451 RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIF
501 QKDINCERYYSFIHLSFQEFFAAMYYILDEGEGGAGPDQDVTRLLTEYAF
551 SERSFLALTSRFLFGLLNEETRSHLEKSLCWKVSPHIKMDLLQWIQSKAQ
601 SDGSTLQQGSLEFFSCLYEIQEEEFIQQALSHFQVIVVSNIASKMEHMVS
651 SFCLKRCRSAQVLHLYGATYSADGEDRARCSAGAHTLLVQLRPERTVLLD
701 AYSEHLAAALCTNPNI ELSLYRNALGSRGVKLLCQGLRHPNCKLQNLRL
751 KRCRISSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHPQC
801 RLQMIQLRKQLESQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQ
851 GLRHPVCRLRTLWLWLDSCGLTAKACENLYFTLGINQTLTDLYLTNNALG
901 DTGVRLLCRLSHPGCKLRVLWLFGM DLNKMTHSRLAALRVTKPYLDIGC
(SEQ ID NO:6)

FIG. 6I

1 ATTGGTGAGTGGGGCAGGGCAGGAGGGAACTGAAGAGTGAGAAAGCATT
51 TTTCAGCAAAAGGTCTTTCTCCCTTGCTCACTCCTCCAACCACTGGCTC
101 AGCCTCTCCGCCCCGCTGCCTGTGAATGATGCAATGGAAGGTGTGCTGGGG
151 TCGCCCTGTGTCCCGTGCATAGGAGCATCTCAGCCTCCAGGTCCTCTCCT
201 TTGGGGCTTACGGCACCCCCATGCTACGAACCGCAGGCAGGGACGGCCTC
251 TGTGCGCTGTCCACCTACTTGAAGAAGCTCGAGGCTGTGGAAGTGAAGAA
301 GTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAAGGCAAGATCC
351 CCTGGGGAAGCATGGAGAAGGCCGGTCCCCTGGAAATGGCCCAGCTGCTC
401 ATCACCCACTTCGGGCCAGAGGAGGCCTGGAGGTTGGCTCTCAGCACCTT
451 TGAGCGGATAAACAGGAAGGACCTGTGGGAGAGAGGACAGAGAGAGGACC
501 TGGTGAGGGATACCCACCTGGTGGCCCGTCCCTCACTTGGGAACCAAGTCA
551 ACATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAAGATCCCCAGGA
601 AACCTACAGGGACTATGTCCGCAGGAAATTCGGGCTCATGGAAGACCGCA
651 ATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC
701 CTGCTGGTGAAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCT
751 GGACACAGGCCGGGGACACGCGAGGACCGTGGGACACCAGGCTAGCCCCA
801 TCAAGATAGAGACCCTCTTTGAGCCAGACGAGGAGCGCCCCGAGCCACCG
851 CGCACCGTGGTCATGCAAGGCGCGGCAGGGATAGGCAAGTCCATGCTGGC
901 ACACAAGGTGATGCTGGACTGGGCGGACGGGAAGCTCTTCCAAGGCAGAT
951 TTGATTATCTCTTCTACATCAACTGCAGGGAGATGAACCAGAGTGCCACG
1001 GAATGCAGCATGCAAGACCTCATCTTACAGCTGCTGGCCTGAGCCCCAGCGC
1051 GCCTCTCCAGGAGCTCATCCGAGTTCCCGAGCGCCTCCTTTTTCATCATCG
1101 ACGGCTTCGATGAGCTCAAGCCTTCTTTCCACGATCCTCAGGACCTTGG
1151 TGCCTCTGCTGGGAGGAGAAACGGCCACGAGCTGCTTCTTAACAGCTT
1201 AATTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACCACACGGC
1251 CCACGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGCACCCCAAGCATGTG
1301 GAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCTACAAGTA
1351 TTTCCACAATGCAGAGCAGGCGGGCCAAGTCTTCAATTACGTGAGGGACA
1401 ACGAGCCTCTCTTACCATGTGCTTCGTCCCCCTGGTGTGCTGGGTGGTG
1451 TGTACCTGCCTCCAGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGAC
1501 GTCCAGGACCACCACTGCAGTGTACATGCTCTACCTGCTGAGTCTGATGC
1551 AACCCAAGCCGGGGGGCCCCGCGCCTCCAGCCCCACCCAACCAGAGAGGG
1601 TTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCCTATTTGA
1651 GGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCT
1701 TCCTCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGTACTAC
1751 AGCTTCATCCACTTGAGTTTCCAGGAATTCTTTGCAGCTATGTACTATAT
1801 CCTGGACGAGGGGGAGGGCGGGGCAGGCCAGACCAGGACGTGACCAGGC
1851 TGTTGACCGAGTACGCGTTTTCTGAAAGGAGCTTCCTGGCACTCACCAGC
1901 CGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAA
1951 GAGTCTCTGCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGCAGT
2001 GGATCCAAAGCAAAGCTCAGAGCGACGGCTCCACCCTGCAGCAGGGCTCC
2051 TTGGAGTTCTTCAGCTGCTTGTACGAGATCCAGGAGGAGGAGTTTATCCA
2101 GCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTGCCTCCA
2151 AGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCGCC
2201 CAGGTGCTGCACTTGTATGGCGCCACCTACAGCGCGGACGGGGAAGACCG
2251 CGCGAGGTGCTCCGCAGGAGCGCACACGCTGTTGGTGCAGCTCAGACCAG
2301 AGAGGACCGTTCTGCTGGACGCCTACAGTGAACATCTGGCAGCGGCCCTG
2351 TGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAAATGCCCTGGG
2401 CAGCCGGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCAACTGCA
2451 AACTTCAGAACCTGAGGCTGAAGAGGTGCCGCATCTCCAGCTCAGCCTGC
2501 GAGGACCTCTCTGCAGCTCTCATAGCCAATAAGAATTTGACAAGGATGGA

2551 TCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCTTTGCGAGG
2601 GCCTGCGGCATCCCCAGTGCAGGCTGCAGATGATTGAGTTGAGGAAGTGT
2651 CAGCTGGAGTCCGGGGCTTGTGAGGAGATGGCTTCTGTGCTCGGCACCAA
2701 CCCACATCTGGTTGAGTTGGACCTGACAGGAAATGCACTGGAGGATTTGG
2751 GCCTGAGGTTACTATGCCAGGGACTGAGGCACCCAGTCTGCAGACTACGG
2801 ACTTTGTGGTGGTTATTTGGGATGGACCTGAATAAAATGACCCACAGTAG
2851 GTTGGCAGCGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGAA
2901 TGGTCCTATCTGCTGGCTCTCCCTGAGATCTGGACAGAGGAAGATGGGA
2951 GGGTGCTCATCACCCCCCAGCATAATGATCAGCCTCCTTCCTAGAGACA
3001 GACTCATGCAGATTGAGATCAAAAGTCCCTCTGCTTGGGATCAAATTAAT
3051 GTTTGACAGAGCTGGCCAGGCGTGGTGGCTCATGTATGTAATCCTAGCAC
3101 TTCGAGAGGCCGAGGCAGGTGGATCACGAGGTCAGGAGTTTGAGATTAGC
3151 CTGGCCAAGATGGTGAAACCCTGTCTCTACTAAAAATAAAAAAAATTAG
3201 CCAGGAAAAAAAAAAAAAAAAA (SEQ ID NO:7)

FIG. 6K

1 MLRTAGRDGLCRLSTYLEELEAVELEKKFKLYLGTATELGEGKIPWGSMEK
51 AGPLEMAQLLITHFGPEEAWRLALSTFERINRKDLWERGQREDLVRDTPP
101 GGPSSLGNQSTCLLEVSLVTPRKDPQETYRDYVRRKFRLMEDRNARLGEC
151 VNLSHRYTRLLLVKEHSNPMQVQQQLLDTGRGHARTVGHQASPIKIETLF
201 EPDEERPEPPRTVVMQGAAGIGKSMLAHKVMLDWADGKLFQGRFDYLFYI
251 NCREMNQSATECSMQDLIFSCWPEPSAPLQELIRVPERLLFIIDGFDELK
301 PSFHDPOGPWCCLWEEKRPTLLLNSLIRKKLLPELSLLITRPTALEKL
351 HRLLEHPRHVEILGFSEAERKEYFYKYFHNAEQAGQVFNYVRDNEPLFTM
401 CFVPLVCWVVCTCLQQQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKPGAP
451 RLQPPPNQRGLCSLAADGLWNQKILFEEQDLRKHGLDGEDVSAFLNMNIF
501 QKDINCERYYSFIHLSFQEFFAAMYIILDEGEGGAGPDQDVTRLLTEYAF
551 SERSFLALTSRFLFGLLNEETRSHLEKSLCWKVSPHIKMDLLQWIOSKAQ
601 SDGSTLQQGSLEFFSCLYEIQEEEFIQQALSHFQVIVVSNIASKMEHMVS
651 SFCLKRCRSAQVLHLYGATYSADGEDRARCSAGAHTLLVQLRPERTVLLD
701 AYSEHLAAALCTNPNIELSRYRNALGSRGVKLLCQGLRHPNCKLQNLRL
751 KRCRISSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLLCEGLRHPQC
801 RLQMIQLRKQCLESQACQEMASVLGTNPHLVELDLTGNALEDLGLRLLCQ
851 GLRHPVCRLRTLWWLFGMDLNKMTSRLAALRVTKPYLDIGC
(SEQ ID NO:8)

FIG. 6L

Rec'd PCT/PTO 21 OCT 2004

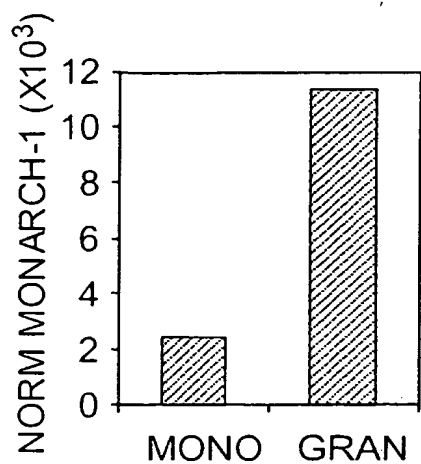


FIG. 7A

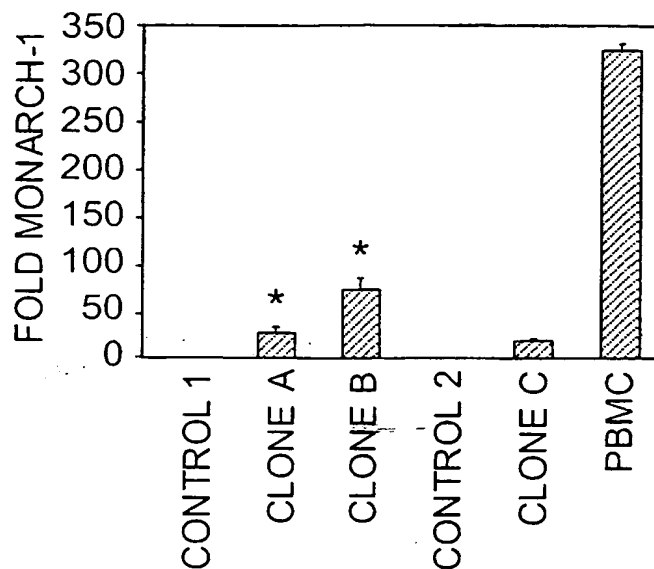


FIG. 8

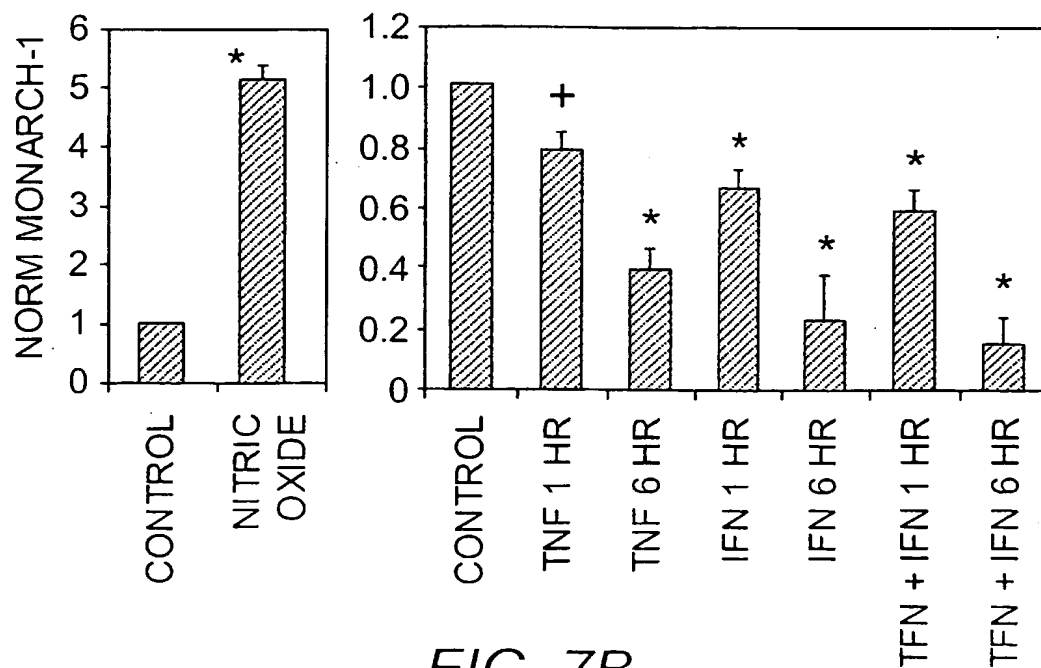


FIG. 7B

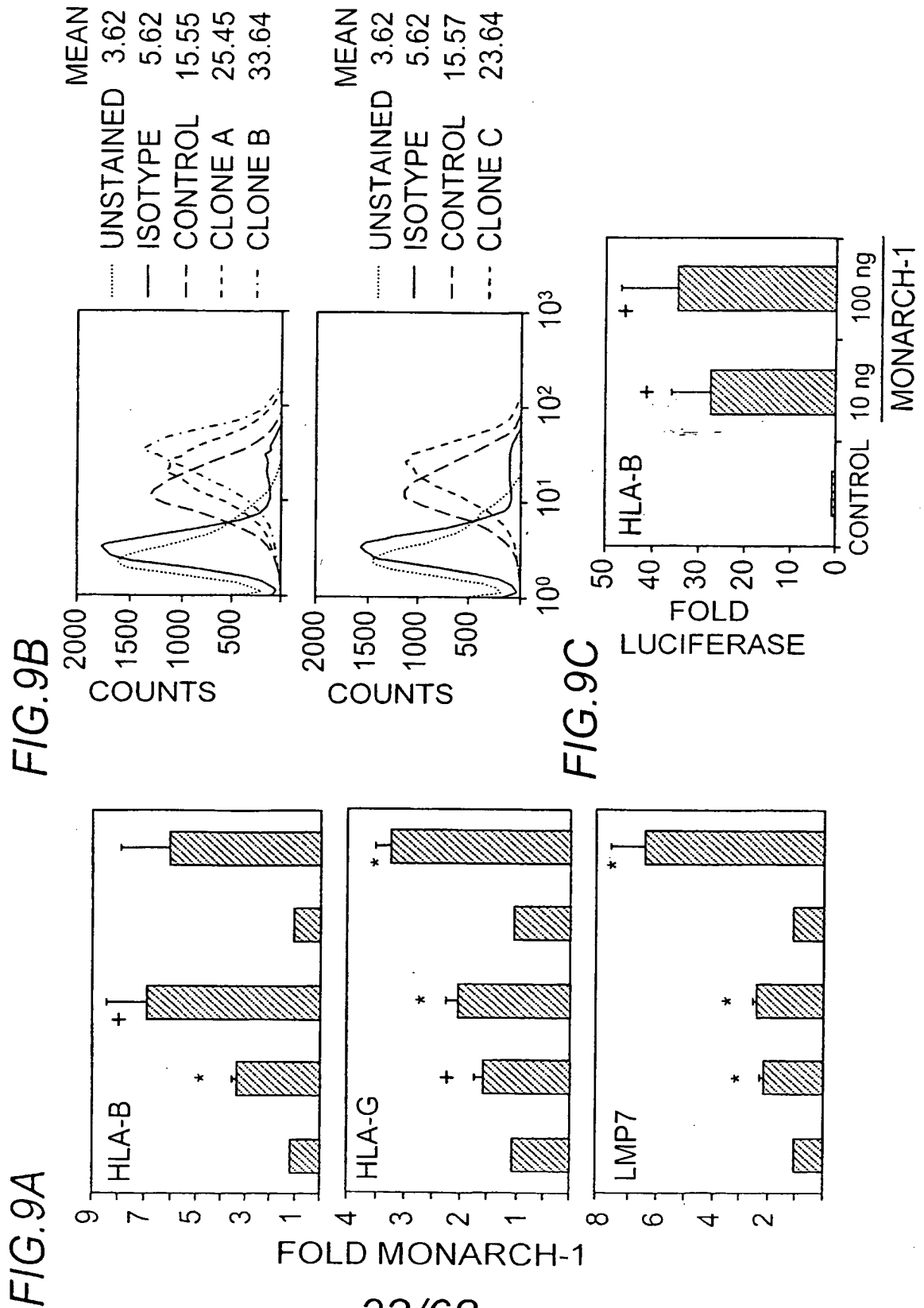


FIG. 10B

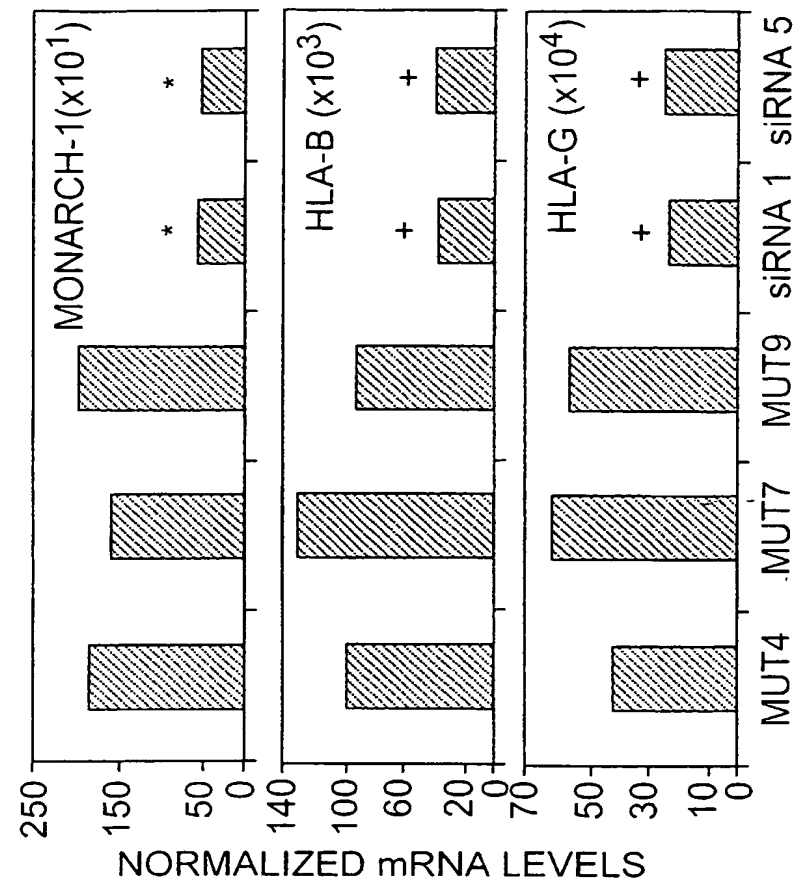
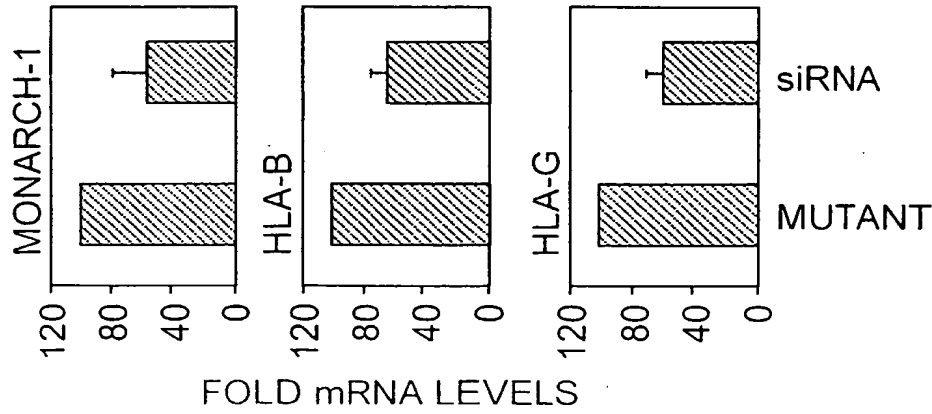
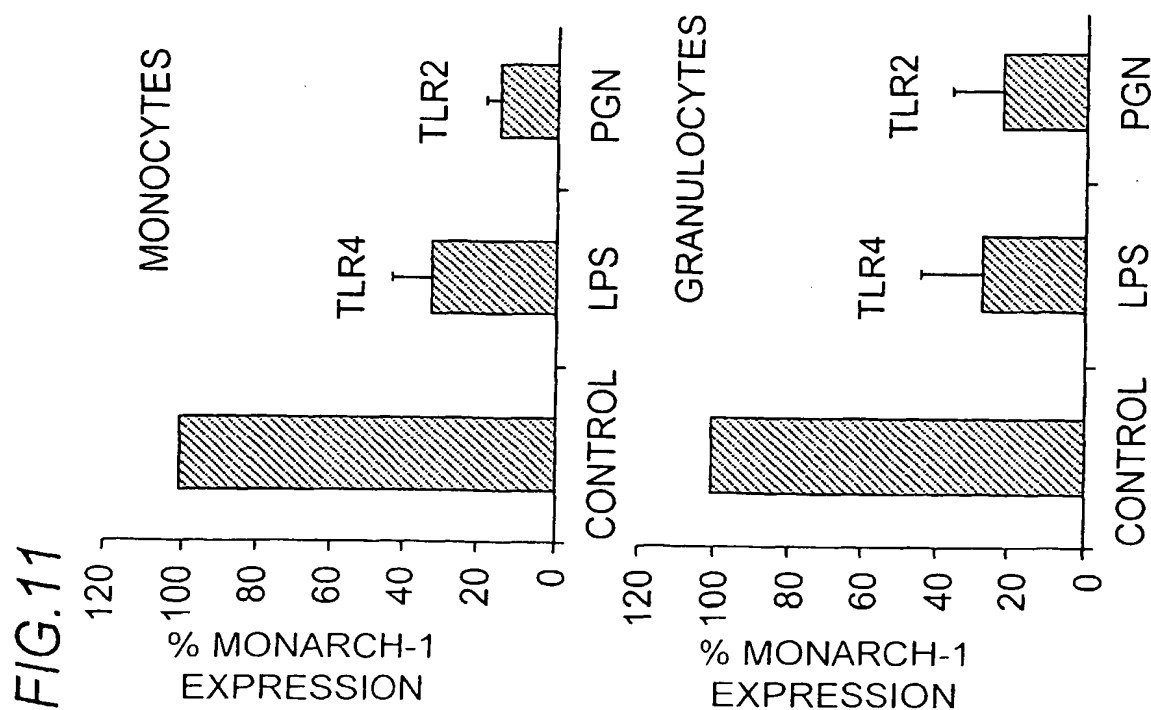
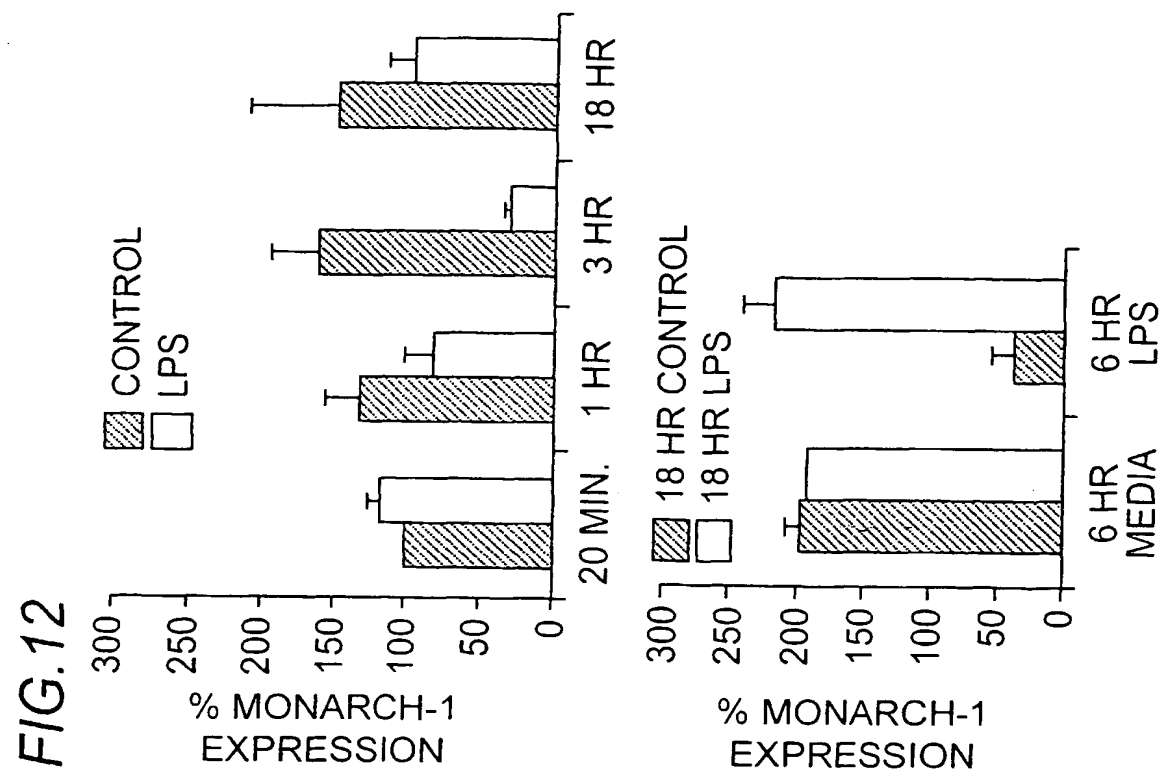


FIG. 10A





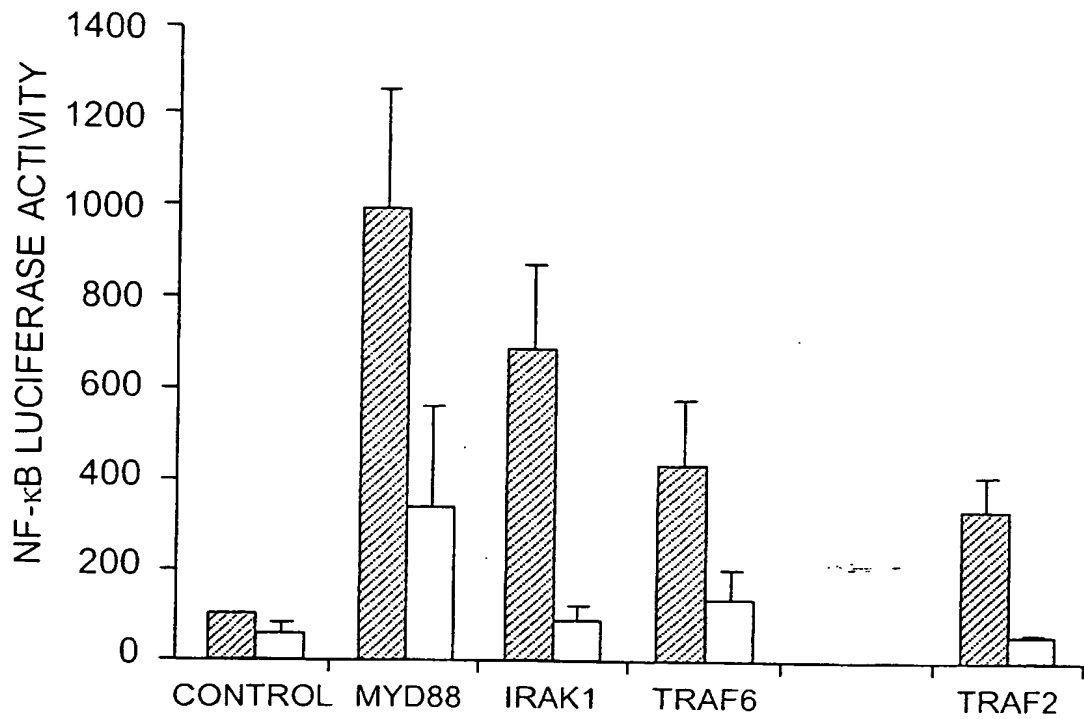
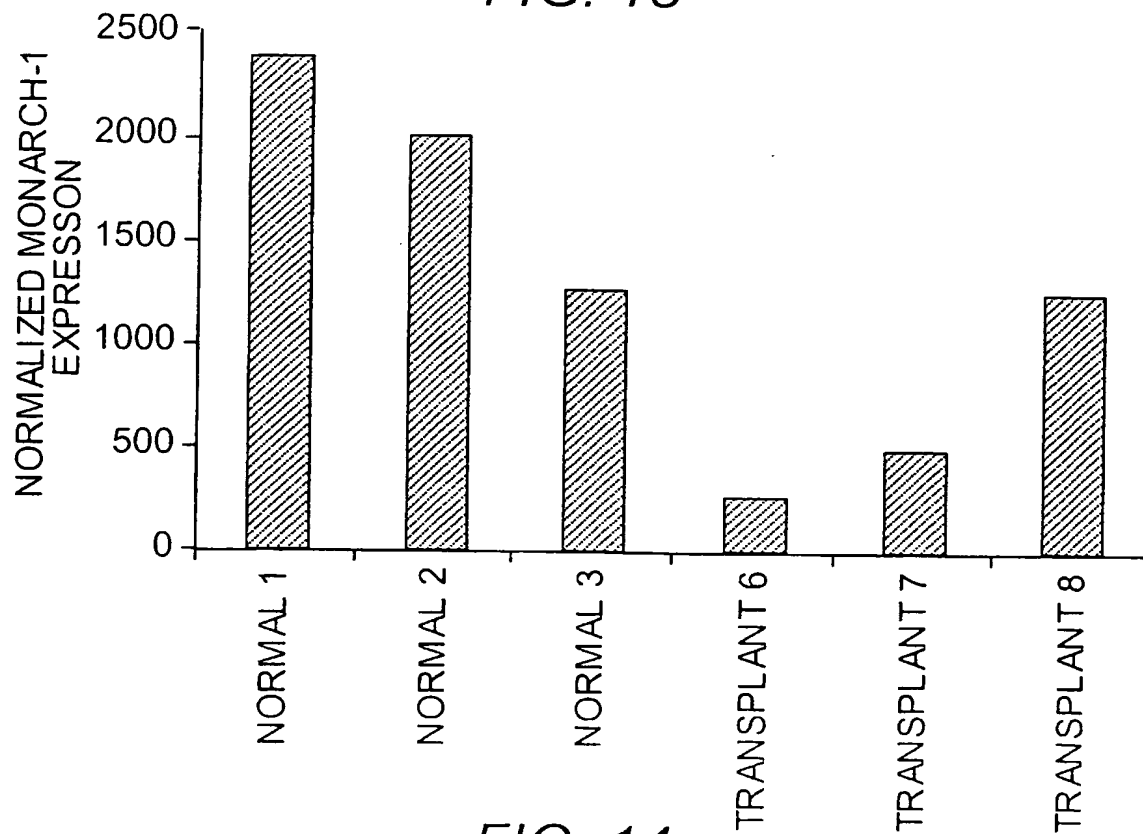


FIG. 13

FIG. 14
25/68

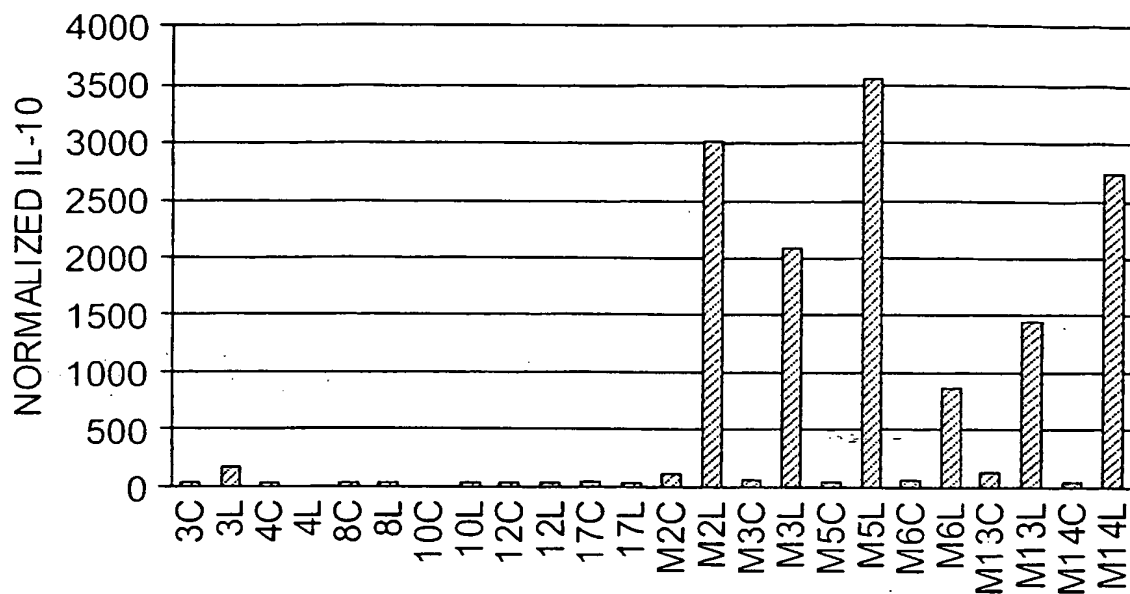


FIG. 15

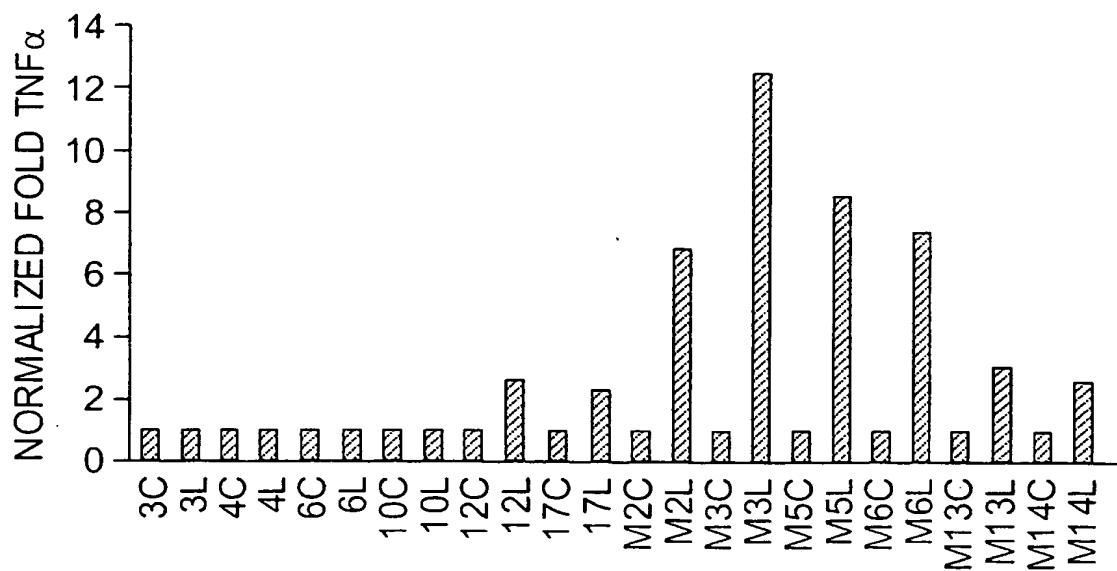
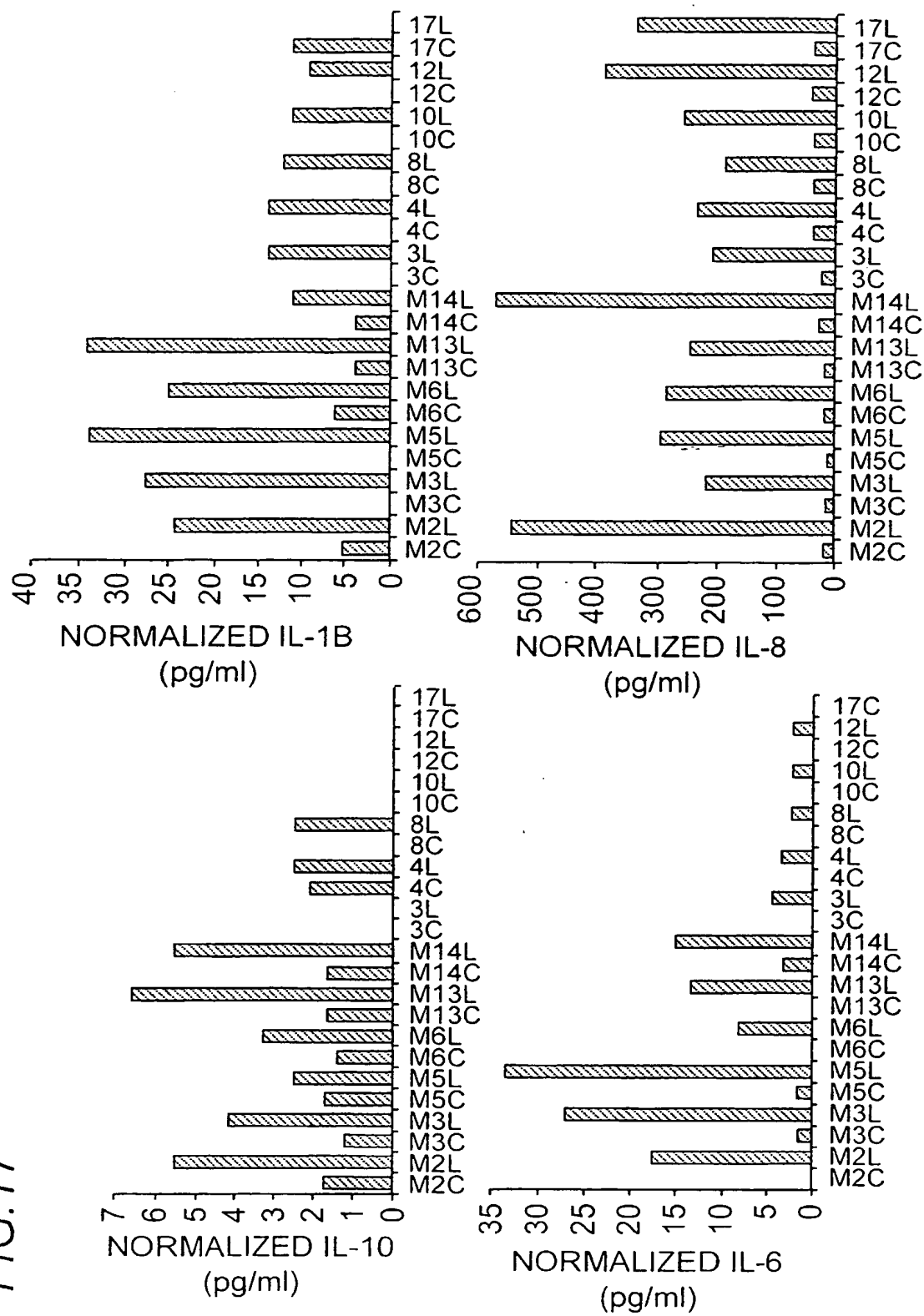


FIG. 16



1 ATGTTGCCGTCTACAGCCAGGGATGGCCTCTATCGACTGTCTACCTACCT
51 GGAAGAACTCGAGGCTGGGGAAGTGAAGAAATTCAAATTATTCTGGGGA
101 TTGCAGAGGACCTGAGCCAGGACAAAATTCCCTGGGGACGAATGGAGAAG
151 GCTGGTCCTCTGGAAATGGCTCAGCTGATGGTGGCCACATGGGGACAAG
201 GGAGGCTTGGCTTCTGGCTCTCAGCACCTTTCAGAGGATTCACAGGAAGG
251 ACCTGTGGGAGCGAGGACAGGGAGAAGACCTGGTGAGGGGTAAGGAGGGC
301 AAGGGAGATCTACAGACAACCTACAAAGACTATGTCCGAAGGAAATTTCCA
351 GCTAATGGAAGACCGCAATGCACGATTAGGCGAATGTGTGAACCTGAGCA
401 ATCGTTACACTCGGCTTCTCCTAGTAAAAGAACTCAAATCCTATCTGG
451 ACACAGCAGAAATTTGTAGATGTAGAGTGGGAACGCTCCAGAACCAGGCG
501 TCACCAGACTAGTCCTATCCAAATGGAGACCCTCTTTGAGCCAGACGAAG
551 AACGCCCCGAGCCACCACACACAGTGGTATTACAAGGGGCGAGCGGGGATG
601 GGGAAAGTCCATGCTGGCCCAAAAGTGATGTTGGACTGGGCCGATGGGAG
651 GCTCTTCCAAGGCCGGTTTGATTATGTCTTCTATATCAGCTGCAGGGAGT
701 TGAATAGAAGCCACACCCAGTGCAGTGTACAAGACCTCATCTCCAGCTGC
751 TGGCCGGAGCGTGGTATATCCCTCGAAGACCTCATGCAGGCTCCTGACCG
801 TCTCCTATTTCATTGATGGCTTCGATAAACTCCATCCTTCTTTCCATG
851 ATGCTCAGGGTCCCTGGTGCCTCTGCTGGGAGGAGAAACAACCTACTGAA
901 GTCCTCCTCGGAAGTCTGATTTCGGAGGTTGCTTCTGCCCCAGGTCTCTCT
951 GCTCATCACACACGACCCTGTGCACTGGAGAAGCTGCACGGCTTGCTAG
1001 AACACCCCAGGCACGTGGAGATCCTGGGCTTCTCCGAGGAAGCTAGGAAG
1051 GAATATTTCTACAGATATTTCCACAACACTGGACAAGCAAGCCGGGTGTT
1101 AAGCTTCTTGATGGACTATGAGCCCCCTCTTTACCATGTGTTTTGTTCCCA
1151 TGGTGTCTGGGTGGTCTGCACCTGCCTAAAGCAGCAGCTGGAAAGTGGG
1201 GAGCTTTTAAGACAAACACCTAGGACCACACAGCTGTTTATATGTTCTA
1251 CCTTCTGAGCCTGATGCAGCCCAAGCCAGGGACTCCAACCTTCAAAGTCC
1301 CAGCCAACCAGAGAGGCCTGGTCTCTCTGGCTGCAGAGGGCCTCTGGAAT
1351 CAGAAGATTCTATTTGATGAACAGGATCTTGGGAAACACGGCCTAGATGG
1401 AGCAGATGTGTCCACTTTTCCTCAACGTGAACATATTCCAGAAGGGTATCA
1451 AATGTGAGAAATTCTACAGCTTCATCCACCTGAGTTTCCAGGAATTCTTC
1501 GCAGCCATGTACTGTGCACTGAATGGCAGAGAGGCGGTGAGGAGAGCGCT
1551 GGCTGAGTATGGTTTTTCGGAAAGGAACTTCTTGGCCCTCACGGTCCACT
1601 TTCTGTTTGGCCTCCTCAACGAAGAGATGAGATGCTACCTTGAGAGGAAT
1651 CTCGGCTGGAGCATCTCCCCTCAGGTGAAGGAGGAAGTGTGGCATGGAT
1701 CCAAAACAAGGCTGGGAGTGAAGGCTCCACCCTGCAGCATGGCTCCCTGG
1751 AGCTACTCAGCTGCTTGTATGAGGTCCAGGAGGAGGACTTCATCCAGCAG
1801 GCCCTGAGCCACTTTCAAGTGGTTGTAGTCAGAAGCATCTCAACAAAGAT
1851 GGAGCACATGGTCTGCTCGTTTTGTGCGAGGTATTGCAGAAGTACAGAAG
1901 TGCTTCACTTGCAATGGGAGTGCTTATAGTACAGGCATGGAGGACGACCCA
1951 CCAGAACCTTCAGGAGTCCAGACTCAGTCCACATACTTACAGGAAAGGAA
2001 CATGCTGCCTGATGTCTACAGTGCATACCTTTTCAGCAGCTGTCTGTACCA
2051 ACTCCAACCTGATCGAGCTGGCCTTATACCGAAATGCCTTGGGCAGCCAG
2101 GGTGTAAGGCTGCTCTGTCAAGGCCTCCGACATGCCAGCTGCAAGCTGCA
2151 GAACCTGAGGCTGAAGAGGTGTGAGATCTCCGGATCAGCCTGCCAGGACC
2201 TCGCAGCCGCTGTTCATCGCCAACAGGAATTTAATCAGGCTGGACCTCAGT
2251 GACAACAGCATTGGGGTGCCAGGCCTGGAGCTGCTCTGTGAGGGGCTGCA
2301 GCACCCAGGTGTAGGCTGCAGATGATCCAGCTGAGGAAGTGTCTGTTGG
2351 AGGCTGCAGCTGGCCGATCCCTGGCTTCTGTTCTCAGCAACAACATCATAT
2401 CTGGTAGAAGTGGATCTGACAGGAAACCCCTTGGAAGATTCGGGGCTGAA
2451 GTTACTGTGTCAAGGGCTAAGGCACCCTGTCTGCAGGCTGCGTACCCTGT
2501 GGCTGAAGATCTGCCACCTTGGACAAGCTTCCCTGCGAAGATCTGGCCTCT

2551 ACTCTCAAAATGAACCAGAGCCTGCTGGAGCTGGACCTGGGTCTGAATGA
2601 TCTTGAGATTCTGGGGTGCTTCTGCTGTGTGAAGGCCTCAGTCATCCAG
2651 ATTGCAAACCTCCAGACCCTTCGGTTGGGCATTTGCCGACTGGGCTCAGTC
2701 GCGTGTGTGGGGATCGCCAGTGTGCTCCAGGTCAACACATGCCTCCAAGA
2751 GCTGGACCTGAGCTTCAATGACTTGGGAGACAGGGGCCTGCAGCTGCTGG
2801 GGGAAGGCCTGAGGCACCAGACCTGCAGACTCCAGAAGCTGTGGCTGGAC
2851 AACTGCGGACTCACCTCCAAAGCATGTGAGGACCTTTCTTCTATCCTGGG
2901 AATCAGCCAGACCCTGCATGAGCTTTATTTGACCAATAATGCTCTGGGGG
2951 ACACAGGTGTCTGTCTGCTGTGCAAGAGGCTGAGGCATCCAGGCTGCAAG
3001 CTTGAGTCTGTGGCTGTTTGGGATGGACCTGAATAAAAAGACTCACAG
3051 GAGGATGGCAGCACTTCGAGTCACAAAACCGTACCTGGATATTGGGTGTT
3101 GA (SEQ ID NO:9)

FIG. 18B

1 MLPSTARDGLYRLSTYLEELEAGELKKFKLFLGIAEDLSQDKIPWGRMEK
51 AGPLEMAQLMVAHMGTTREAWLLALSTFQRIHRKDLWERGQGEDLVRGKEG
101 KGDLOTYKDYVRRKFQLMEDRNARLGECVNLSNRYTRLLLVKEHSNPIW
151 TQQKFVDVEWERSRTRRHQTSPIQMETLFEPDEERPEPPHTTVVLQGAAGM
201 GKSM LAHKVMLDWADGRLFQGRFDYVFYISCRELNRSHTQCSVQDLISSC
251 WPERGISLEDLMQAPDRLLFIIDGFDKLHPSFHDAQGPWCLCWECKQTE
301 VLLGSLIRLLLPQVSLLITTRPCALEKLHGLLEHPRHVEILGFSEEARK
351 EYFYRYFHNTGQASRVLSFLMDYEPLFTMCFVPMVSWVCTCLKQQLESG
401 ELLRQTPRTTTAVYMFYLLSLMQPKPGTPTFKVPANQRGLVSLAAEGLWN
451 QKILFDEQDLGKHGLDGADVSTFLNVNIFQKGIKCEKFYSFIHLSFQEFF
501 AAMYCALNGREAVRRALA EYGFSEFNFLALT VHFLFGLLNEEMRCYLERN
551 LGWSISPVKEEVLAWIQNKAGSEGSTLQHGSLELLSCLYEVEEDFIQQ
601 ALSHFQVVVRSISTKMEH MVCSFCARYCRSTEVLHLHGSAYSTGMEDDP
651 PEP SGVQTQSTYLQERNMLPDVYSAYLSAAVCTNSNLI ELALYRNALGSQ
701 GVRLLCQGLRHASCKLQNLRLKRCQISGSACQDLAAAVIANRNLIRLDLS
751 DNSIGVPGLELLCEGLQHPRCRLQMIQLRKCLLEAAAGRSLASVLSNNSY
801 LVELDLTGNPLEDSGLKLLCQGLRHPVCRLRTLWLKICH LGQASCEDLAS
851 TLKMNQSLLELDLGLNDLGDSGVLLLC EGLSHPDCKLQTLRLGICRLGSV
901 ACVG IASVLQVNTCLQELDLSFNDLGDRGLQLLGEGLRHQTCRLQKLWLD
951 NCGLTSKACEDLSSILGISQTLHELYLTNNALGDTGVCLLCKRLRHPGCK
1001 LRLVWLFGMDLNKKTHRRMAALRVTKPYLDIGC (SEQ ID NO:10)

FIG. 18C

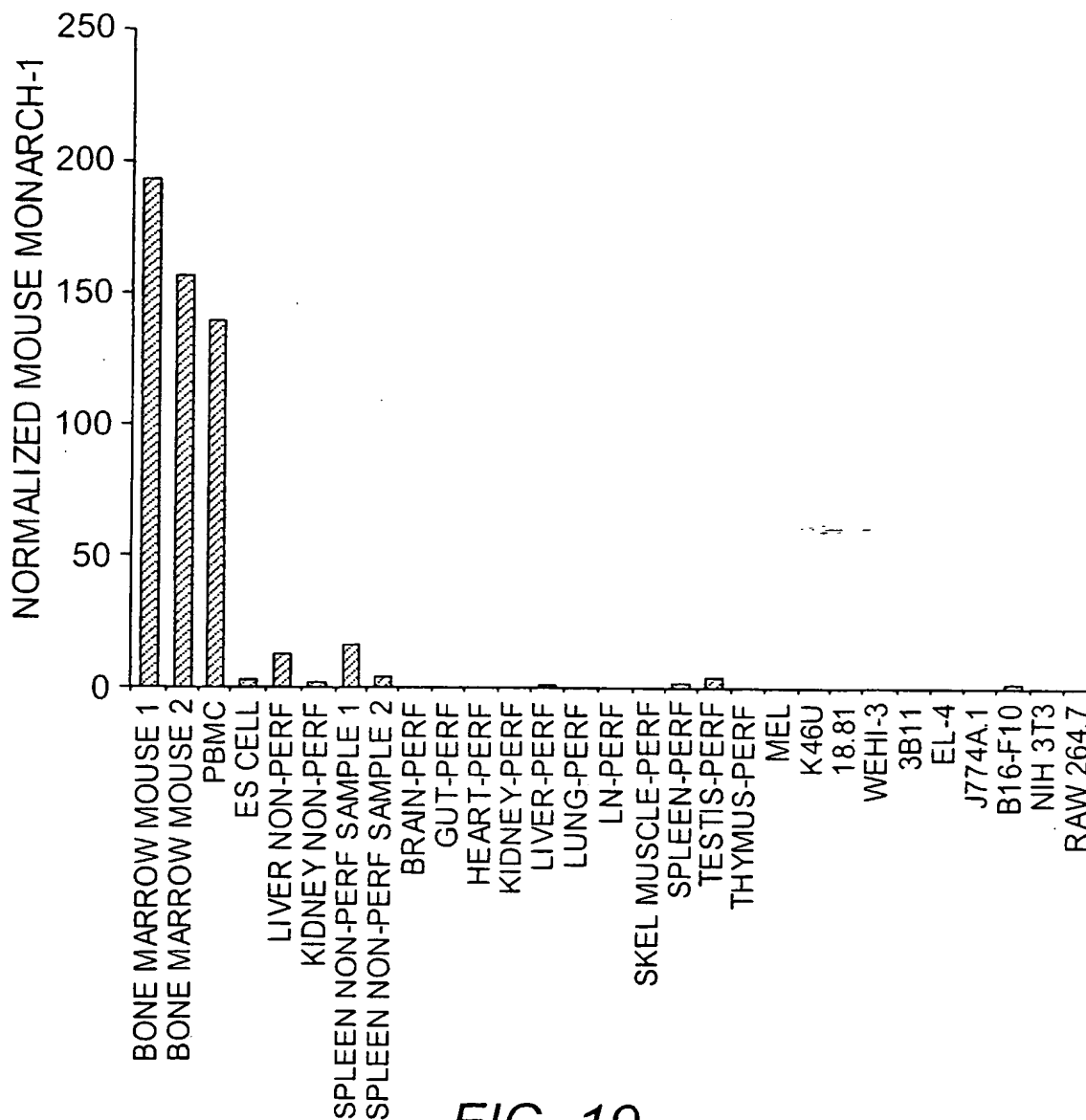


FIG. 19

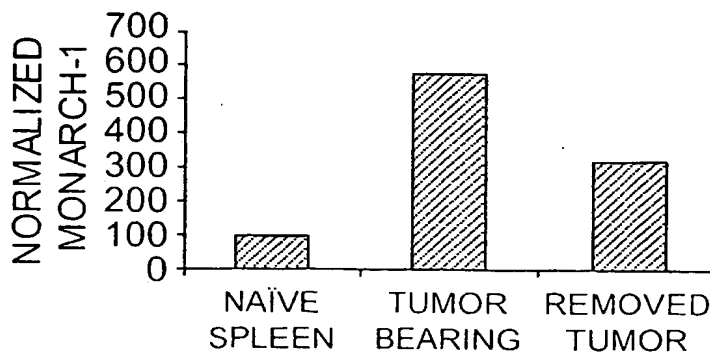


FIG. 20

1 ATGGCAGATTTCATCATCATCTTCTTTCTTTCCTGATTTTGGGCTGCTATT
51 GTATTTGGAGGAGCTAAACAAAGAGGAATTAAATACATTCAAGTTATTCC
101 TAAAGGAGACCATGGAACCTGAGCATGGCCTGACACCCTGGAATGAAGTG
151 AAGAAGGCCAGGCGGGAGGACCTGGCCAATTTGATGAAGAAATATTATCC
201 AGGAGAGAAAGCCTGGAGTGTGTCTCTCAAAATCTTTGGCAAGATGAACC
251 TGAAGGATCTGTGTGAGAGAGCGAAAGAAGAGATCAACTGGTTCGGCCCAG
301 ACTATAGGACCAGATGATGCCAAGGCTGGAGAGACACAAGAAGATCAGGA
351 GGCAGTGGTGGGTGATGGAACAGAATACAGAAATAGAATAAAGGAAAAAT
401 TTTGCATCACTTGGGACAAGAAGTCTTTGGCTGGAAAGCCTGAAGATTTTC
451 CATCATGGAATTGCAGAGAAAGATAGAAAACCTGTTGGAACACTTGTTCGA
501 TGTGGATGTCAAAACCGGTGCACAGCCACAGATCGTGGTGCTTCAGGGAG
551 CTGCTGGAGTTGGGAAAACAACCTTGGTGAGAAAGGCAATGTTAGATTGG
601 GCAGAGGGCAGTCTCTACCAGCAGAGGTTTAAAGTATGTTTTTTATCTCAA
651 TGGGAGAGAAATTAACCAGCTGAAAGAGAGAAGCTTTGCTCAATTGATAT
701 CAAAGGACTGGCCCAGCACAGAAGGCCCCATTGAAGAAATCATGTACCAG
751 CCAAGTAGCCTCTTGTTTATTATTGACAGTTTCGATGAACTGAACTTTGC
801 CTTTGAAGAACCTGAGTTTGCAGTGTGCGAAGACTGGACCCAAGAACACC
851 CAGTGTCTTCTCATGAGTAGTTTGCTGAGGAAAGTGATGCTCCCTGAG
901 GCATCCTTATTGGTGACAACAAGACTCACAACCTTCTAAGAGACTAAAGCA
951 GTTGTTGAAGAATCACCATTATGTAGAGCTACTAGGAATGTCTGAGGATG
1001 CAAGAGAGGAGTATATTTACCAGTTTTTTGAAGATAAGAGGTGGGCCATG
1051 AAAGTATTTCAGTTCATAAAAAGCAATGAGATGCTGTTTAGCATGTGCCA
1101 AGTCCCCCTAGTGTGCTGGGCCGCTTGTACTTGTCTGAAGCAGCAAATGG
1151 AGAAGGGTGGTGATGTACATTGACCTGCCAAACAACCACAGCTCTGTTT
1201 ACCTGCTATATTTCTAGCTTGTTTCACACCAGTAGATGGAGGCTCTCCTAG
1251 TCTACCCAACCAAGCCCAGCTGAGAAGACTGTGCCAAGTCGCTGCCAAAG
1301 GAATATGGACTATGACTTACGTGTTTTACAGAGAAAAATCTCAGAAGGCTT
1351 GGGTTAACTCAATCTGATGTCTCTAGTTTTATGGACAGCAATATTATTCA
1401 GAAGGACGCAGAGTATGAAAACCTGCTATGTGTTTCACCCACCTTCATGTTT
1451 AGGAGTTTTTTGTCAGCTATGTTCTATATGTTGAAAGGCAGTTGGGAAGCT
1501 GGGAAACCCTTCTGCCAGCCTTTTGAAGATTTGAAGTCATTACTTCAAAG
1551 CACAAGTTATAAAGACCCCCATTTGACACAGATGAAGTGCTTTTTTGTGTTG
1601 GCCTTTTGAATGAAGATCGAGTAAACAACCTGGAGAGGACTTTTAACTGT
1651 AAAATGTCAGTGAAGATAAAATCAAAGTTACTTCAGTGTATGGAAGTATT
1701 AGGAAACAGTGACTATTCTCCATCACAGCTGGGATTTCTGGAGTTGTTTC
1751 ACTGTCTGTATGAGACTCAAGATAAAGCGTTTTATAAGCCAGGCAATGAGA
1801 TGTTTCCCAAAGGTTGCCATTAATATTTGTGAGAAAATACATTTGCTTGT
1851 ATCTTCTTTCTGCCTTAAGCACTGCCGGTGTTTGCGGACCATCAGGCTGT
1901 CTGTAACCTGTGGTATTTGAGAAGAAGATATTA AAAACAAGCCTCCCAACT
1951 AACACTTGGTTGAAATTTATCACTTTCCCTGATGGTTGTCAGGATATCTC
2001 TACTTCTTTGATTTCATAACAAGAATCTGATGCATCTTGACCTAAAAGGGA
2051 GTGATATAGGGGATAATGGAGTAAAGTCATTGTGTGAGGCCTTGAAACAC
2101 CCAGAGTGTAACCTACAGACTCTCAGGCTGGAATCTTGCAACCTAACTGT
2151 ATTTTGTGTCTAAATATATCTAATGCTCTCATCAGAAGCCAGAGCCTGA
2201 TATTTCTGAATCTGTCAACCAATAATCTGTTGGATGATGGAGTGCAGCTT
2251 TTGTGTGAGGCCTTAAGACATCCAAAGTGTTATCTAGAGAGACTGTCCTT
2301 AGAAAGCTGTGGTCTCACAGAGGCTGGCTGTGAGTATCTTTCTTTGGCTC
2351 TCATCAGCAATAAAAGACTGACACATTTGTGCTTGGCAGACAATGTCTTG
2401 GGTGATGGTGGAGTAAAGCTTATGAGTGATGCCCTGCAACATGCACAATG
2451 TACTCTGAAGAGCCTTGTGCTGAGGCGTTGCCATTTCACTTCACTTAGCA

2501 GTGAATATCTGTCAACTTCTCTTCTACACAACAAGAGCCTGACGCATCTG
2551 GATCTAGGATCAAACCTGGCTACAAGACAATGGAGTGAAGCTTCTGTGTGA
2601 TGTCTTTCGGCATCCAAGCTGTAATCTTCAGGACTTGGAATTGATGGGCT
2651 GTGTTCTCACTAATGCATGTTGTCTGGATCTGGCTTCTGTTATTTTGAAT
2701 AACCCAAACCTGAGGAGCCTGGACCTTGGAACAACGATTTGCAGGATGA
2751 TGGAGTGAAAATTCTGTGTGATGCTTTGAGATATCCAACTGTAAACATTC
2801 AGAGGCTCGGGTTGGAATACTGTGGTTTGACATCTCTCTGCTGTCAAGAT
2851 CTCTCCTCTGCTCTTATCTGCAACAAAAGACTGATAAAAATGAATCTGAC
2901 ACAGAATACCTTAGGATATGAAGGAATTGTGAAGTTATATAAAGTCTTGA
2951 AGTCTCCTAAGTGTAAGTACAAGTTCTAGGACAACAGGATTTCCAAGCT
3001 GCCCAAGGAAAACCTCCAACAAAGAGCTGGCTCTGGATGA
(SEQ ID NO:11)

FIG. 21B

1 MADSSSSSFFPDFGLLLYLEELNKEELNTFKLFLKETMEPEHGLTPWNEV
51 KKARREDLANLMKKYYPGEKAWSVSLKIFGKMNLKDLCEAKEEINWSAQ
101 TIGPDDAKAGETQEDQEAVLGDGTEYRNRIKEKFCITWDKKS LAGKPEDF
151 HHGIAEKDRKLLLEHLFDVDVKTGAQPQIVVLQGAAGVGKTTLVKAMLDW
201 AEGSLYQQRFKYVFYLN GREINQLKERSFAQLISKDWPSTEGPIEEIMYQ
251 PSSLLFIIDSFDELNF AFEEPEFALCEDWTQEHVPSFLMSSLLRKVMLPE
301 ASLLVTTRLTTSKRLKQLLKNHHYVELLGMSEDAREEYIYQFFEDKRWAM
351 KVFSSLKSNEMLFSMCQVPLVCWAACTCLKQQMEKGGDVTLTCQTTTALF
401 TCYISSLFTPVDGGSPSLPNQAQLRRLCQVAAKGIWTMTYVFYRENLRRL
451 GLTQSDVSSFMDSNIIQKDAEYENCYVFTHLHVQEFFAAMFYMLKGSWEA
501 GNPSCQPFEDLKSLLQSTS YKDPHLTQMKCFLFGLLNEDRVKQLERTFNC
551 KMSLKI KSKLLQCM EVLGNSDYSPSQLGFLELFHCLYETQDKAFISQAMR
601 CFPKVA INICEKIHLLVSSFCLKHCRCLRTIRLSVTTVVFEKKILKTSLPT
651 NTWLKFITFPDGCQDI STSLIHNKNLMHLDLKGSDIGDNGVKS LCEALKH
701 PECKLQTLRLESCNLT VFCCLNISNALIRSQSLIFLNLSTNNLLDDGVQL
751 LCEALRHPKCYLERLSLESCGLTEAGCEYLSLALISNKRLTHLCLADNVL
801 GDGGVKLMSDALQHAQCT LKSLVLRCHFTSLSSEYLSLSTSLHKNKSLTHL
851 DLGSNWLQDNGVKLLCDVFRHPSCNLQDLELMGCVLTNACCLDLASVILN
901 NPNLRSLDLGNNDLQDDGVKILCDALRYPCNIIQRLGLE YCGLTSLCCQD
951 LSSALICNKRLIKMNL TQNTLGYEGIVKLYKVLKSPKCKLQVLGQQDFQA
1001 AQGKLQQRAGSG (SEQ ID NO:12)

FIG. 21C
32/68

1 ATGGCAGATTCATCATCATCTTCTTTCTTTCTTCTGATTTTGGGCTGCTATT
51 GTATTTGGAGGAGCTAAACAAAGAGGAATTAAATACATTCAAGTTATTCC
101 TAAAGGAGACCATGGAACCTGAGCATGGCCTGACACCCTGGAATGAAGTG
151 AAGAAGGCCAGGCGGGAGGACCTGGCCAATTTGATGAAGAAATATTATCC
201 AGGAGAGAAAGCCTGGAGTGTGTCTCTCAAATCTTTGGCAAGATGAACC
251 TGAAGGATCTGTGTGAGAGAGCGAAAGAAGAGATCAACTGGTCGGCCCAG
301 ACTATAGGACCAGATGATGCCAAGGCTGGAGAGACACAAGAAGATCAGGA
351 GGCAGTGCTGGGTGATGGAACAGAATACAGAAATAGAATAAAGGAAAAAT
401 TTTGCATCACTTGGGACAAGAAGTCTTTGGCTGGAAAGCCTGAAGATTTTC
451 CATCATGGAATTGCAGAGAAAGATAGAAAACCTGTTGGAACACTTGTTCGA
501 TGTGGATGTCAAAACCGGTGCACAGCCACAGATCGTGGTGCTTCAGGGAG
551 CTGCTGGAGTTGGGAAAACAACCTTGGTGAGAAAGGCAATGTTAGATTGG
601 GCAGAGGGCAGTCTCTACCAGCAGAGGTTTAAGTATGTTTTTTATCTCAA
651 TGGGAGAGAAATTAACCAGCTGAAAGAGAGAAGCTTTGCTCAATTGATAT
701 CAAAGGACTGGCCCAACACAAAAGCCCCCATTGAAGAAATCATGTACCAG
751 CCAAGTAGCCTCTTGTTTTATTATAGACAGTTTCGATGAACTGAACTTTGC
801 CTTTGAAGAACCTGAGTTTGCACCTGTGCGAAGACTGGACCCAAGACAACC
851 CATGTCTCTTCTCATGAGTAGTTTGCTGAGGAAAGTGATGCTCCCTGAG
901 GCATCCTTATTGGTGACAACAAGACTCACAACTTCTAAGAGACTAAAGCA
951 GTTGTTGAAGAATCACCATTATGTAGAGCTACTAGGAATGTCTGAGGATG
1001 CAAGAGAGGAGTATATTTACCAGTTTTTTGAAGATAAGAGGTGGGCCATG
1051 AAAGTATTCAGTTCACTAAAAAGCAATGAGATGCTGTTTAGCATGTGCCA
1101 AGTCCCCCTAGTGTGCTGGGCCGCTTGTAAGTGTCTGAAGCAGCAATGG
1151 AGAAGGGTGCTGATGTCACATTGACCTGCCAAACAACCACAGCTCTGTTT
1201 ACCTGCTATATTTCTAGCTTGTTTACACCAGTAGATGGAGGCTCTCCTAG
1251 TCTACCCAACCAAGCCCAGCTGAGAAGACTGTGCCAAGTCGCTGCCAAAG
1301 GAATATGGACTATGACTTACGTGTTTTACAGAGAAAATCTCAGAAGGCTT
1351 GGGTTAACTCAATCTGATGTCTCTAGTTTTTATGGACAGCAATATTATTCA
1401 GAAGGACGCAGAGTATGAAAACCTGCTATGTGTTTACCCACCTTCATGTTT
1451 AGGAGTTTTTTGTCAGCTATGTTCTATATGTTGAAGGGCAGTTGGGAAGCT
1501 GGGAAACCCTTCTGCCAGCCTTTTGAAGATTTGAAGTCATTACTTCAAAG
1551 CACAAGTTATAAAGACCCCCATTTGACACAGATGAAGTGCTTTTTTGTTT
1601 GCCTTTTGAATGAAGATCGAGTAAACAACCTGGAGAGGACTTTTAACTGT
1651 AAAATGTCACTGAAGATAAAATCAAAGTTACTTCAGTGTATGGAAGTATT
1701 AGGAAACAGTGACTATTCTCCATCACAGCTGGGATTTCTGGAGTTGTTTC
1751 ACTGTCTGTATGAGACTCAAGATAAAGCGTTTATAAGCCAGGCAATGAGA
1801 TGTTTCCCAAAGGTTGCCATTAATATTTGTGAGAAAATACATTGGCTTGT
1851 ATCTTCTTTCTGCCTTAAGCACTGCCGATGTTTGCAGACCATCAGGCTGT
1901 CTGTAAGTGTGCTATTTGAGAAGAAGACATTAAAAACAAGCCTCCCAACT
1951 AACACTTGGGATGGTGATCGCATTACTCACTGTTGGAAAGATCTCTGTTT
2001 TGTGCTTCATACAAATGAACACTTGAGAGAATTGGACCTGTACCATAGCA
2051 ACCTTGATAAATCAGCAATGAATATCCTGCATCATGAACTAAGCCACCCA
2101 AACTGTAACTACAAAACTACTGTTGAAATTTATCACTTTCCCTGATGG
2151 TTGTCAGGATATCTCTACTTCTTTGATTACATAACAAGAATCTGATGCATC
2201 TTGACCTAAAGGGAGTGATATAGGGGATAATGGAGTAAAGTCATTGTGT
2251 GAGGCCTTGAAACACCCAGAGTGTAAGTACAGACTCTCAGCTTAGAAAG

FIG. 21D

33/68

2301 CTGTGGTCTCACAGAGGCTGGCTGTGAGTATCTTTCTTTGGCTCTCATCA
2351 GCAATAAAAGACTGACACATTTGTGCTTGGCAGACAATGTCTTGGGTGAT
2401 GGTGGAGTAAAGCTTATGAGTGATGCCCTGCAACATGCACAATGTACTCT
2451 GAAGAGCCTTGTGCTGAGGCGTTGCCATTTCACTTCACTTAGCAGTGAAT
2501 ATCTGTCAACTTCTCTTCTACACAACAAGAGCCTGACGCATCTGGATCTA
2551 GGATCAAACCTGGCTACAAGACAATGGAGTGAAGCTTCTGTGTGATGTCTT
2601 TCGGCATCCAAGCTGTAATCTTCAGGACTTGAATTGATGGGCTGTGTTT
2651 TCACTAATGCATGTTGTCTGGATCTGGCTTCTGTTATTTTGAATAACCCA
2701 AACCTGAGGAGCCTGGACCTTGGGAACAACGATTTGCAGGATGATGGAGT
2751 GAAAATTCTGTGTGATGCTTTGAGATATCCAAACTGTAACATTCAGAGGC
2801 TCGGGTGA (SEQ ID NO:13)

FIG. 21E

1 MADSSSSSFFPDFGLLLYLEELNKEELNTFKLFLKETMEPEHGLTPWNEV
51 KKARREDLANLMKKYYPGEKAWSVSLKIFGKMNLKDLCEAKEEINWSAQ
101 TIGPDDAKAGETQEDQEAVLGDGTEYRNRIKEKFCITWDKKS LAGKPEDF
151 HHGIAEKDRKLLLEHLFDVDVKTGAQPQIVVLQGAAGVGKTTLVRKAMLDW
201 AEGSLYQQRFKYVFYLN GREINQLKERSFAQLISKDWPNTKAPIEEIMYQ
251 PSSLLFIIDSFDELNF AFEPEFALCEDWTQDNPVSFLMSSLLRKVMLPE
301 ASLLVTTRLTTSKRLKQLLKNHHYVELLGMS EDAREEYIYQFFEDKRWAM
351 KVFSSLKSNEMLFSMCQVPLVCWAACTCLKQOMEKGGDVT LTCQTTTALF
401 TCYISSLFTPV DGGSPSLPNQAQLRRLCQVAAKGIWTMTYVFYRENLRRL
451 GLTQSDVSSFMD SNI IQKDAEYENCYVFTHLHVQEFFAAMFYMLKGSWEA
501 GNPSCQPFEDLKSLLQSTSYKDPH LTQMKCFLFGLLNEDRVKQLERTFNC
551 KMSLKI KSKLLQCM EVLGNSDYSPSQLGFLELFHCLYETQDKAFISQAMR
601 CFPKVAINICEK IHWLVSSFCLKHCRCLQTIRLSVTVLFEKKTLKTS LPT
651 NTWDGDRITHC WKDLC SVLHTNEHLRELDLYHSNLDKSAMN ILHHEL SHP
701 NCKLQKLLLKFITFPDGCQDISTSLIHNKNLMHLDLKGSDIGDNGV KSLC
751 EALKHPECKLQ TLSLESCGLTEAGCEYLSLALISNKRLTHLCLADNV LGD
801 GGVKLMSDALQHAQCTLKSLVLR RCHFTSLSSEYLS TSL LHNKSLTHL DL
851 GSNWLQDNGVKLLCDVFRHPS CNLQDLELMGCVLTNACCLDLASVILN NP
901 NLRSLDLGNNDLQDDGVKILCDAL RYPNCNIQRLG (SEQ ID NO:14)

FIG. 21F

FIG. 22

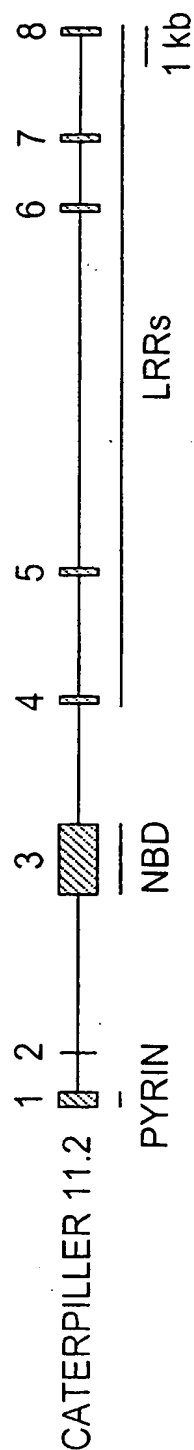


FIG. 23A

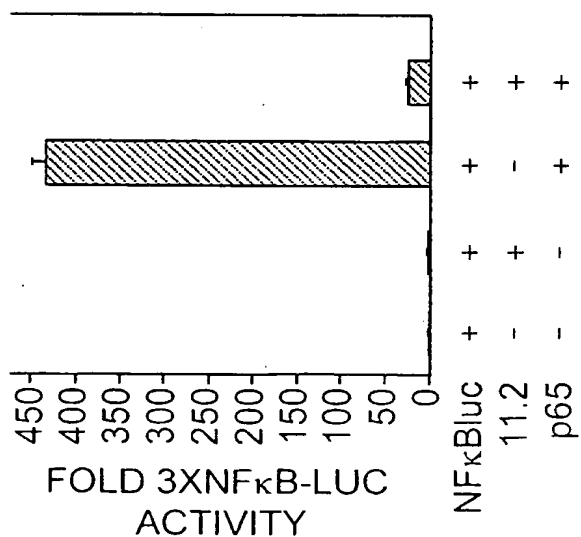


FIG. 23B

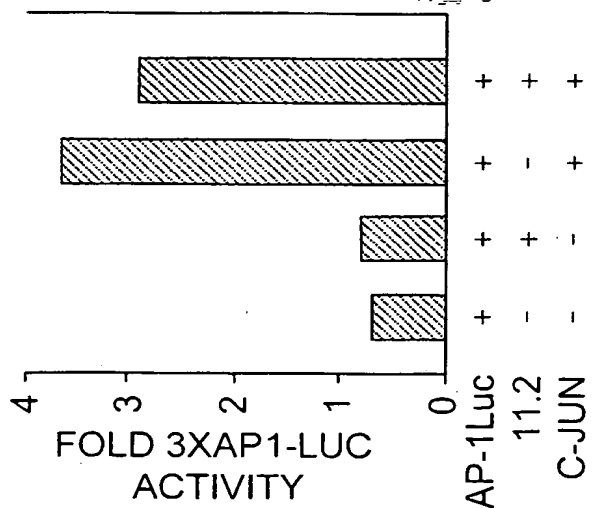
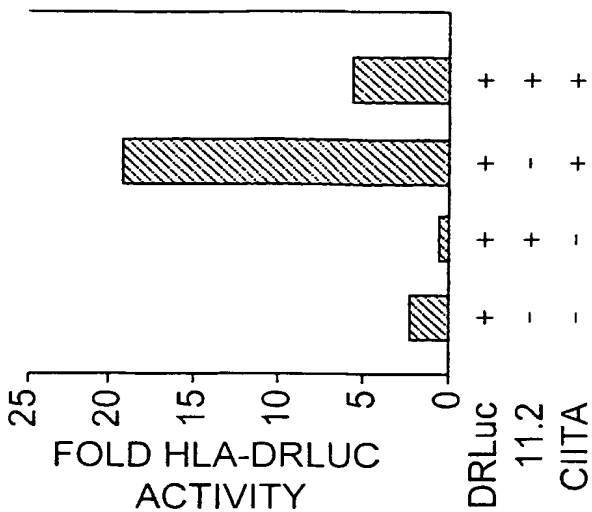


FIG. 24



Rec'd PCT/PTO 21 OCT 2004

1 AAGCTATACAGCGGCACCGCCGGAACCTGGCTGAGTGGTTCAGCCGGCTG
51 CCCAGGGAGGAGCGCCAGTTTGGCCCAACCTTTGCCCTAGACACGGTCCA
101 CGTTGACCCTGTGATCCGCGAGAGTACCCCTGATGAGCTACTTCGCCCCAC
151 CCGCGGAGCTGGCCTTGGAGCATCAGCCACCCCAGGCCGGGCTCCCCCA
201 CTGGCCTTGTCTCAGCTCTTTAACCCGGATGCCTGTGGGCGCCGGGTGCA
251 GACAGTGGTGTCTGTATGGGACAGTGGGCACAGGCAAGAGCACGCTGGTGC
301 GCAAGATGGTTCTGGAAGTGGTGTATGGGCGGCTGCCGGCCTTCGAGCTG
351 CTCATCCCCTTCTCCTGTGAGGACCTGTCTATCCCTGGGCCCTGCCCCAGC
401 CTCCCTGTGCCAACTTGTGGCCCAGCGCTACACGCCCTTGAAGGAGGTTT
451 TGCCCCCTGATGGCTGCTGCTGGGTCCCACCTCCTCTTTGTGCTCCATGGC
501 TTAGAGCATCTCAACCTCGACTTCCGGCTGGCAGGCACGGGACTTTGTAG
551 TGACCCGGAGGAACCGCAGGAACCAGCTGCTATCATCGTCAACCTGCTGC
601 GCAAATACATGCTGCCTCAGGCCAGCATTCTGGTGACCACTCGGCCCTCT
651 GCCATTGGCCGTATCCCCAGCAAGTACGTGGGCGGCTATGGTGAGATCTG
701 CGGTTTCTCTGATACCAACCTGCAGAAGCTCTACTTCCAGCTCCGCCTCA
751 ACCAGCCGTACTGCGGGTATGCCGTTGGCGGTTTCAGGTGTCTCTGCCACA
801 CCAGCTCAGCGTGACCACCTGGTGCAGATGCTCTCCCGGAACCTGGAGGG
851 GCACCACCAGATAGCCGCTGCCTGCTTCCCTGCCGTCTATTGCTGGCTCG
901 TTTGTGCCACCTTGCACCTTCTGCTATGCCCCACGCGTGETGGGCAGACC
951 CTTACAAGCATCTATACCAGCTTCCCTGCGCCTCAACTTCAGCGGGGAAAC
1001 CTTGGACAGCACTGACCCCTCCAATTTGTCCCTGATGGCCTATGCAGCCC
1051 GAACCATGGGCAAGTTGGCCTATGAGGGGGTGTCTCCCGCAAGACCTAC
1101 TTCTCTGAAGAGGATGTCTGTGGCTGCCTGGAGGCTGGCATCAGGACGGA
1151 GGAGGAGTTTCAGCTGCTGCACATCTTCCGTCGGGATGCCCTGAGGTTTT
1201 TCCTGGCCCCATGTGTGGAGCCAGGGCGTGCAGGCACCTTCGTGTTTACC
1251 GTGCCCCGATGCAGGAATACCTGGCTGCCCTCTACATTGTGCTGGGTTT
1301 GCGCAAGACGACCCTGCAAAAGGTGGGCAAGGAAGTGGCTGAGCTCGTGG
1351 GCCGTGTTGGGGAGGACGTACGCTGGTACTGGGCATCATGGCCAAGCTG
1401 CTGCCTCTGCGGGCTCTGCCTCTGCTCTTCAACCTGATCAAGGTGGTTCC
1451 ACGAGTGTGTTGGGCGCATGGTGGGTAAGGCGGGAGGCGGTGGCTCAGG
1501 CCATGGTGCTGGAGATGTTTCGAGAGGAGGACTACTACAACGATGATGTT
1551 CTGGACCAGATGGGCGCCAGTATCCTGGGCGTGGAGGGCCCCCGGCGCCA
1601 CCCAGATGAGCCCCCTGAGGATGAAGTCTTCGAGCTCTTCCCCATGTTCA
1651 TGGGGGGCTTCTCTCTGCCACACCGAGCTGTGCTAGCTCAGCTTGGC
1701 TGCCCCATCAAGAACCTGGATGCCCTGGAGAATGCCAGGCCATCAAGAA
1751 GAAGCTGGGCAAGCTGGGCGGGCAGGTGCTGCCCCCATCAGAGCTCCTTG
1801 ACCACCTCTTCTTCCACTATGAGTTCAGAACAGCGCTTCTCCGCTGAG
1851 GTGCTCAGCTCCCTGCGTCAGCTCAACCTGGCAGGTGTGCGCATGACACC
1901 AGTCAAGTGCACAGTGGTGGCAGCTGTGCTGGGCGAGCGGAAGGCATGCCC
1951 TGGATGAGGTGAACCTGGCCTCCTGCCAGCTAGATCCTGCTGGGCTGCGC
2001 ACACTCCTGCCTGTCTTCTGCGTGCCCGGAAGCTGGGCTTGCAACTCAA
2051 CAGCCTGGGCCCTGAGGCCTGCAAGGACCTCCGAGACCTGTTGCTGCATG
2101 ACCAGTGCCAAATTACCACACTGCGGCTGTCCAACAACCCGCTGACGGCG
2151 GCAGGCCTGGAGCTGCTGGCTGCCAGCTGGACCGCAACCGGCAGCTGCA
2201 GGAGCTGAACGTGGCGTACAACGGTGTGCTGGTGACACAGCGGCCCTGGCCC
2251 TGGCCAGAGCTGCCCGGGAGCACCTTCCCTGGAAGTGTCTACAAGCTCTA
2301 CTGAATGGCATCGACTTTCTCTCTCCTGCCAGCCTTACTTCAATGAGCT
2351 GAGCTCAGAGGGCCGCCAGGTCTTGCGAGACTTGGGGGTGCTGCTGAAG
2401 GTGGTGCCCGGGTGGTGGTGTACTGACAGAGGGGACGGCGGTGTGAGAA
2451 TACTGGTCAGTGATCCTCAGTGAAGTCCAGCGGAACCTCAATAGCTGGGA
2501 TCGGGCCCCGGTTTCAGCGACACCTTGAAGCTCCTACTGCGGGATCTGGAAG
2551 ATAGCCGGGGTGCCACCCTTAATCCTTGGCGCAAGGCCAGCTGCTGCGA
2601 GTGGAGGGCGAG (SEQ ID NO:15)

FIG. 25A
36/68

1 AIQRHRRNLAEWFSRLPREERQFGPTFALDTPVHVDPVIRESTPDELLRPP
 51 AELALEHQPPQAGLPPLALSQLFNPDACGRRVQTVVLYGTVGTGKSTLVR
 101 KMLVDWCYGRLPAPFELLIPFSCEDLSSLGPAPASLCQLVAQRYTPLKEVL
 151 PLMAAAGSHLLFVLHGLEHLNLDLFRLAGTGLCSDPEEPQEPAAIIVNLLR
 201 KYMLPQASILVTTRPSAIGRIPSKYVGRYGEICGFSDTNLQKLYFQLRLN
 251 QPYCGYAVGGSGVSATPAQRDHLVQMLSRNLEGGHQIAAACFLPSYCWL
 301 CATLHFLHAPTPAGQTLTSIYTSFLRLNFSGETLDSTDPNSLSLMAYAAR
 351 TMGKLAYEGVSSRKTYFSEEDVCGCLEAGIRTEEEFQLLHIFRRDALRFF
 401 LAPCVEPGRAGTFVFTVPAMQEYLAALYIVLGLRKTTLQKVGKEVAELVG
 451 RVGEDVSLVLGIMAKLLPLRALPLLFNLIKVVPRVFGRMVGKSREAVAQA
 501 MVLEMFREEDYINDDVLDQMGASILGVEGPRRHPDEPPEDEVFELFPMFM
 551 GLLSAHNRAVLAQLGCPIKNLDALENAQAIKKKLGLGRQVLPPSELDD
 601 HLFHFEYFQNRFSAEVLSSLRQLNLGVRMTPVKCTVVA AVLGSGRHAL
 651 DEVNLASCQLDPAGLRTLLPVFLRARKLGLQLNSLGPEACKDLRDLRLH
 701 QCQITTLRLSNPLTAAGLELLAAQLDRNRQLQELNVAYNGAGDTAALAL
 751 ARAAREHPSLELLQALLNGIDFLSPASLYFNELSSEGRQVLRDLGGAAEG
 801 GARVVVSLTEGTAVSEYWSVILSEVQRNLNSWDRARVQRHLELLLRDLED
 851 SRGATLNPWRKAQLLRVEGE (SEQ ID NO:16)

FIG. 25B

1 ATGAGGTGGGGCCACCATTTGCCAGGGCCTCTTGGGGCTCTGGTTTTAG
 51 AAGAGCACTCCAGCGACCAGATGATCGTATCCCCTTCTGATCCACTGGA
 101 GTTGGCCCCCTTCAAGGGGAGCGTCCCTTTGGGCCCCCTAGGGCCTTTATA
 151 CGCCACCACGGAAGCTCGGTAGATAGCGCTCCCCCATCCGGGAGGCATGG
 201 ACGGCTGTTCCCCAGCGCCTCTGCAACTGAAGCTATACAGCGGCACCGCC
 251 GGAACCTGGCTGAGTGGTTCAGCCGGCTGCCCAGGGAGGAGCGCCAGTTT
 301 GGCCCAACCTTTGCCCTAGACACGGTCCACGTTGACCCTGTGATCCGCGA
 351 GAGTACCCCTGATGAGCTACTTCGCCCCACCCGCGGAGCTGGCCCTGGAGC
 401 ATCAGCCACCCAGGCCGGGCTCCCCCACTGGCCTTGTCTCAGCTCTTT
 451 AACCCGGATGCCTGTGGGCGCCGGGTGCAGACAGTGGTGCTGTATGGGAC
 501 AGTGGGCACAGGCAAGAGCACGCTGGTGCAGCAAGATGGTTCTGGACTGGT
 551 GTTATGGGCGGCTGCCGGCCTTCGAGCTGCTCATCCCCTTCTCCTGTGAG
 601 GACCTGTCATCCCTGGGCCCTGCCCCAGCCTCCCTGTGCCAACTTGTGGC
 651 CCAGCGCTACACGCCCCCTGAAGGAGTTCTGCCCCCTGATGGCTGCTGCTG
 701 GGTCCACCTCCTCTTTGTGCTCCATGGCTTAGAGCATCTCAACCTCGAC
 751 TTCCGGCTGGCAGGCACGGGACTTTGTAGTGACCCGGAGGAACCGCAGGA
 801 ACCAGCTGCTATCATCGTCAACCTGCTGCGCAAATACATGCTGCCTCAGG
 851 CCAGCATTCTGGTGACCACTCGGCCCTCTGCCATTGGCCGTATCCCCAGC
 901 AAGTACGTGGGCGGCTATGGTGAGATCTGCGGTTTCTCTGATACCAACCT
 951 GCAGAAGCTCTACTTCCAGCTCCGCCTCAACCAGCCGTAAGTGGGGTATG
 1001 CCGTTGGCGGTTTCAGGTGTCTCTGCCACACCAGCTCAGCGTGACCACCTG
 1051 GTGCAGATGCTCTCCCGGAACCTGGAGGGGCACCACCAGATAGCCGCTGC
 1101 CTGCTTCCTGCCGTCTATTGCTGGCTCGTTTGTGCCACCTTGCACTTCC
 1151 TGCATGCCCCCAGCCTGCTGGGCAGACCCTTACAAGCATCTATACCAGC
 1201 TTCCTGCGCCTCAACTTCAGCGGGGAAACCCTGGACAGCACTGACCCCTC
 1251 CAATTGTCCCTGATGGCCTATGCAGCCCCGAACCATGGGCAAGTTGGCCT
 1301 ATGAGGGGTGTCCTCCCGCAAGACCTACTTCTCTGAAGAGGATGTCTGT
 1351 GGCTGCCTGGAGGCTGGCATCAGGACGGAGGAGGAGTTTCAGCTGCTGCA

FIG. 25C

1451 CATCTTCCGTCGGGATGCCCTGAGGTTTTTCTGGCCCCATGTGTGGAGC
1501 CAGGGCGTGCAGGCACCTTCGTGTTACCGTGCCCGCCATGCAGGAATAC
1551 CTGGCTGCCCTCTACATTGTGCTGGGTTTGC GCAAGACGACCCTGCAAAA
1601 GGTGGGCAAGGAAGTGGCTGAGCTCGTGGGCCGTGTTGGGGAGGACGTCA
1651 GCCTGGTACTGGGCATCATGGCCAAGCTGCTGCCTCTGCGGGCTCTGCCT
1701 CTGCTCTTCAACCTGATCAAGGTGGTTCACGAGTGTTTGGGCGCATGGT
1751 GGGTAAAAGCCGGGAGGCGGTGACTCAGGCCATGGTGCTGGAGATGTTTC
1801 GAGAGGAGGACTACTACAACGATGATGTTCTGGACCAGATGGGCGCCAGT
1851 ATCCTGGGCGTGGAGGGCCCCCGGCCACCCAGATGAGCCCCCTGAGGA
1901 TGAAGTCTTCGAGCTCTTCCCCATGTTTCATGGGGGGGCTTCTCTCTGCCC
1951 ACAACCGAGCTGTGCTAGCTCAGCTTGGCTGCCCCATCAAGAACCTGGAT
2001 GCCCTGGAGAATGCCAGGCCATCAAGAAGAAGCTGGGCAAGCTGGGCGCG
2051 GCAGGTGCTGCCCCCATCAGAGCTCCTTGACCACCTCTTCTTCCACTATG
2101 AGTTCAGAACACGCGCTTCTCCGCTGAGGTGCTCAGCTCCCTGCGTCAG
2151 CTCAACCTGGCAGGTGTGCGCATGACACCAGTCAAGTGCACAGTGGTGGC
2201 AGCTGTGCTGGGCAGCGGAAGGCATGCCCTGGATGAGGTGAACTTGGCCT
2251 CCTGCCAGCTAGATCCTGCTGGGCTGCGCACACTCCTGCCTGTCTTCCTG
2301 CGTGCCCGGAAGCTGGGCTTGCAACTCAACAGCCTGGGCCCTGAGGCCTG
2351 CAAGGACCTCCGAGACCTGTTGCTGCATGACCAGTGCEAAATTACCACAC
2401 TGCGGCTGTCCAACAACCCGCTGACGGAGGCAGGTGTTGCCGTGCTAATG
2451 GAGGGGCTGGCAGGAAACACCTCAGTGACGCACCTGTCCCTGCTGCACAC
2501 GGGCCTTGGGGACGAAGGCCTGGAGCTGCTGGCTGCCAGCTGGACCGCA
2551 ACCGGCAGCTGCAGGAGCTGAACGTGGCGTACAACGGTGCTGGTGACACA
2601 GCGGCCCTGGCCCTGGCCAGAGCTGCCCGGGAGCACCTTCCCTGGAAC
2651 GCTACACCTCTACTTCAATGAGCTGAGCTCAGAGGGGCCAGGTCTTGC
2701 GAGACTTGGGGGGTGTGCTGCTGAAGGTGGTGCCCGGGTGGTGGTGTCACTG
2751 ACAGAGGGGACGGCGGTGTCAGAATACTGGTCAGTGATCCTCAGTGAAGT
2801 CCAGCGGAACCTCAATAGCTGGGATCGGGCCCGGGTTTACGCGACACCTTG
2851 AGCTCCTACTGCGGGATCTGGAAGATAGCCGGGGTGCCACCCTTAATCCT
2901 TGACGCAAGGCCAGCTGCTGCGAGTGAGGGGCGAGGTCAGGGCCCTCCT
2951 GGAGCAGCTGGGAAGCTCTGGAAGCTGAGACACTGGCGGCAGGCACCTAG
3001 CTATGTGACCACTGGCCCTAAACCTTTTCCCTCTGTGGCCTCCTGGCTTG
3051 CACTGCTCCCTCTAGAA (SEQ ID NO:17)

FIG. 25D

1 MRWGHHLPRASWGSFRRALQRPDDRIPFLIHWSWPLQGERPFGPPRAFI
51 RHHGSSVDSAPPSGRHGR LFP SASATEAIQRHRRNLAEWFSRLPREERQF
101 GPTFALD TVHVDPIRE STPDELLRPPAELALEHQPPQAGLPPLALSOLF
151 NPDACGRRVQTVVLYGT VGTGKSTLVRKMVLWDWCYGR LPAFELLIPFSCE
201 DLSSLGPAPASLCQLVAQRYT PLKEVLPLMAAAGSHLLFVLHGLEHLNLD
251 FRLAGTGLCSDPEEPQEPAAI I VNLLRK YMLPQASILVTTRPSAIGRIPS
301 KYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYAVGGSGVSATPAQRDHL
351 VQMLSRNLEGHHQIAAACFLPSYCWLVCATLHFLHAPTPAGQTLTSIYTS
401 FLRLNFSGETLDSTDP SNLSLMAYAARTMGK LAYEGVSSRKTYFSEEDVC
451 GCLEAGIRTEEEFQLLHIFRRDALRFFLAPC VEPGRAGTFVFTVPAMQ EY
501 LAALYIVLGLRKTTLQKV GKEVAELVGRVGEDVSLVLGIMAKLLPLRALP
551 LLFNLIKVVPRVFGRMV GKSREAVTQAMVLEMFREEDY YNDVDVLDQM GAS
601 ILGVEGPRRHPDEPPEDEV FELPFMFMGGLLSAHNRAVL AQLGCPIKNLD
651 ALENAQAIKKKLGLGRQVLP PSELLDHLFFHYEFQNRQFSAEVLSSLRQ
701 LNLAGVRMTPVKCTVVA AVLGSGRHALDEVN LASCQLDPAGLRTLLPVFL
751 RARKLGLQLNSLGPEACKDL RDLLLDHQCQITTLRLSNNPLTEAGVAVLM
801 EGLAGNTSVTHLSLLHTGL GDEGLELLAAQLDRNRQLQELNVAYNGAGDT
851 AALALARAAREHPSLELLHLYFNELSS EGRQVLRDLGGAAEGGARVVVSL
901 TEGTAVSEYWSVILSEVQRNLNSWDRARVQRHLELLLRDLEDSRGATLNP
(SEQ ID NO:18)

FIG. 25E

Rec'd PCT/PTO 21 OCT 2004

1 ATGAGATGGGGCCACCATTGCCCCAGGGCCTCTTGGGGCTCTGGTTTTAG
51 AAGAGCACTCCAGCGACCAGATGATCGTATCCCCCTTCCTGATCCACTGGA
101 GTTGGCCCCCTTCAAGGGGAGCGTCCCTTTGGGGCCCCCTAGGGCCTTTATA
151 CGCCACCACGGAAGCTCGGTAGATAGCGCTCCCCCATCCGGGAGGCATGG
201 ACGGCTGTTCCCCAGCGCTCTGCAACTGAAGCTATACAGCGGCACCGCC
251 GGAACCTGGCTGAGTGGTTCAGCCGGCTGCCCAGGGAGGAGCGCCAGTTT
301 GGCCCAACCTTTGCCCTAGACACGGTCCACGTTGACCCTGTGATCCGCGA
351 GAGTACCCCTGATGAGCTACTTCGCCCCACCCGCGGAGCTGGCCCTGGAGC
401 ATCAGCCACCCACGGCCGGGCTCCCCCACTGGCCTTGTCTCAGCTCTTT
451 AACCCGGATGCCTGTGGGCGCCGGGTGCAGACAGTGGTGCTGTATGGGAC
501 AGTGGGCACAGGCAAGAGCACGCTGGTGCGCAAGATGGTTCTGGACTGGT
551 GTTATGGGCGGCTGCCGGCCCTTCGAGCTGCTCATCCCCTTCTCCTGTGAG
601 GACCTGTTCATCCCTGGGCCCTGCCCCAGCCTCCCTGTGCCAACTTGTGGC
651 CCAGCGCTACACGCCCCCTGAAGGAGGTTCTGCCCCCTGATGGCTGCTGCTG
701 GGTCCCACCTCCTCTTTGTGCTCCATGGCTTAGAGCATCTCAACCTCGAG
751 TTCGGCTGGCAGGCACGGGACTTTGTAGTGACCCGGAGGAACCGCAGGA
801 ACCAGCTGCTATCATCGTCAACCTGCTGCGCAAATACATGCTGCCTCAGG
851 CCAGCATTCTGGTGACCACTCGGCCCTCTGCCATTGGCCGTATCCCCAGC
901 AAGTACGTGGGCGCTATGGTGAGATCTGCGGTTTCTCTGATACCAACCT
951 GCAGAAAGCTCTACTTCCAGCTCCGCCTCAACCAGCCGTAETGCGGGTATG
1001 CCGTTGGCGGTTTCAAGGTGTCTCTGCCACACCAGCTCAGCGTGACCACCTG
1051 GTGCAGATGCTCTCCCGGAACCTGGAGGGGCACCACCAGATAGCCGCTGC
1101 CTGCTTCCTGCCGTCTTATTGCTGGCTCGTTTGTGCCACCTTGCACCTTCC
1151 TGCATGCCCCCACGCCTGCTGGGCAGACCCTTACAAGCATCTATACCAGC
1201 TTCCTGCGCCTCAACTTCAGCGGGGAAACCCCTGGACAGCACTGACCCCTC
1251 CAATTTGTCCCTGATGGCCTATGCAGCCCGAACCATGGGCAAGTTGGCCT
1301 ATGAGGGGGTGTCTTCCCGCAAGACCTACTTCTCTGAAGAGGATGTCTGT
1351 GGCTGCCTGGAGGCTGGCATCAGGACGGAGGAGGAGTTTTCAGCTGCTGCA
1401 CATCTTCCGTCCGGATGCCCTGAGGTTTTTCTGGCCCCATGTGTGGAGC
1451 CAGGGCGTGCAAGGCACCTTCGTGTTACCCGTGCCCGCCATGCAGGAATAC
1501 CTGGCTGCCCTCTACATTGTGTGGTGGTTTTCGCAAGACGACCCCTGCAAAA
1551 GGTGGGCAAGGAAGTGGCTGAGCTCGTGGGCGGTGTTGGGGAGGACGTCA
1601 GCCTGGTACTGGGCATCATGGCCAAGCTGCTGCCTCTGCGGGCTCTGCCT
1651 CTGCTCTTCAACCTGATCAAGGTGGTTCACGAGTGTTTGGGCGCATGGT
1701 GGGTAAAAGCCGGGAGGCGGTGACTCAGGCCATGGTGCTGGAGATGTTTC
1751 GAGAGGAGGACTACTACAACGATGATGTTCTGGACCAGATGGGCGCCAGT
1801 ATCCTGGGCGTGGAGGGGCCCCCGGCGCCACCCAGATGAGCCCCCTGAGGA
1851 TGAAGTCTTCGAGCTCTTCCCCATGTTTCATGGGGGGGCTTCTCTCTGCC
1901 ACAACCGAGCTGTGCTAGCTAGCTAGCTTGGCTGCCCCATCAAGAACCTGGAT
1951 GCCCTGGAGAATGCCAGGCCATCAAGAAGAAGCTGGGCAAGCTGGGCGG
2001 GCAGGTGCTGCCCCCATCAGAGCTCCTTGACCACCTCTTCTTCCACTATG
2051 AGTTCCAGAACCAGCGCTTCTCCGCTGAGGTGCTCAGCTCCCTGCGTCAG
2101 CTCAACCTGGCAGGTGTGCGCATGACACCAGTCAAGTGCACAGTGGTGGC
2151 AGCTGTGCTGGGCAGCGGAAGGCATGCCCTGGATGAGGTGAACTTGGCCT
2201 CCTGCCAGCTAGATCCTGCTGGGCTGCGCACACTCCTGCCTGTCTTCCTG
2251 CGTGCCCGGAAGCTGGGCTTGCAACTCAACAGCCTGGGCCCTGAGGCCTG
2301 CAAGGACCTCCGAGACCTGTTGCTGCATGACCAGTGCCAAATTACCACAC
2351 TGCGGCTGTCCAACAACCCGCTGACGGAGGCAGGTGTTGCCGTGCTAATG
2401 GAGGGGCTGGCAGGAAACACCTCAGTGACGCACCTGTCCCTGCTGCACAC
2451 GGGCCTTGGGGACGAAGGCCTGGAGCTGCTGGCTGCCAGCTGGACCGCA
2501 ACCGGCAGCTGCAGGAGCTGAACGTGGCGTACAACGGTGTGGTGACACA
2551 GCGGCCCTGGCCCTGGCCAGAGCTGCCCGGGAGCACCCCTTCCCTGGAAC
2601 GCTACAGGGTGTGCGCATCCAGATGTGTTGGAAGCTTCCCCTCCTGCCTT
2651 ATGCTCACCTGTGGACACCGAGGATGCCCTCACATTGGTGCTTTCTCCTC
2701 ATCCTCATGCCCCCTTTGCCACAATGGTATGATGGCTTGGTATGCCCTCG
2751 AGGCAGATGCACCTGACTTGCTGCTATTAAAAAGCCGTGTGCCTTCTACC
(SEQ ID NO:19)

FIG. 25F
39/68

Rec'd PCT/PTO 21 OCT 2004

1 MRWGHHLPRASWGS GFRRALQRPDDRIPFLIHWSWPLQGERPFGPPRAFI
 51 RHHGSSVDSAPPSGRHGR LFPSASATEAIQRHRRNLAEWFSRLPREERQF
 101 GPTFALDTVHVDPVIRESTPDELLRPPAELALEHQPPQAGLPPLALSOLF
 151 NPDACGRRVQTVVLYGT VGTGKSTLVRKMVLDWCYGR LPAFELLIPFSCE
 201 DLSSLGPAPASLCQLVAQRYT PLKEVLPLMAAAGSHLLFVLHGLEHLNLD
 251 FRLAGTGLCSDPEEPQEPAAI IVNLLRKYMLPQASILVTTRPSAIGRIPS
 301 KYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYAVGGSGVSATPAQRDHL
 351 VQMLSRNLEGGHQIAAACFLPSYCWLVCATLHFLHAPT PAGQTLTSIYTS
 401 FLRLNFSGETLDSTDPSNLSLMAYAARTMGKLAYEGVSSRKTYFSEEDVC
 451 GCLEAGIRTEEEFQLLHIFR RDALRFFLAPC VEPGRAGTFVFTVPAMQEY
 501 LAALYIVLGLRKTTLQKVGKEVAELVGRVGEDVSLVLGIMAKLLPLRALP
 551 LLFNLIKVVPRVFGRMVGKSREAVTQAMVLEMFREEDYYNDDVLDQMGAS
 601 ILGVEGPRRHPDEPPEDEVFELFPMFMGGLLSAHNRAVLAQLGCPIKNLD
 651 ALENAQAIKKKLGKLGRQVLPPSELLDHLFFHYEFQNRQFSAEVLSSLRQ
 701 LNLAGVRMTPVKCTVVA AVLGSGRHALDEVNLASCQLDPAGLRTLTPVFL
 751 RARKLGLQLNSLGPEACKDLRDLLLHDQCQITTLRLSNNPLTEAGVAVLM
 801 EGLAGNTSVTHLSLLHTGLGDEGLELLAAQLDRNRQLQELNVAYNGAGDT
 851 AALALARAAREHPSLELLQGVAIQMCWKLP LLYAHLWTPRMP SHWCFL
 901 ILMPLPQWYDGLVAPRGRCT&LAAIKKPCAFY (SEQ ID NO:20)

FIG. 25G

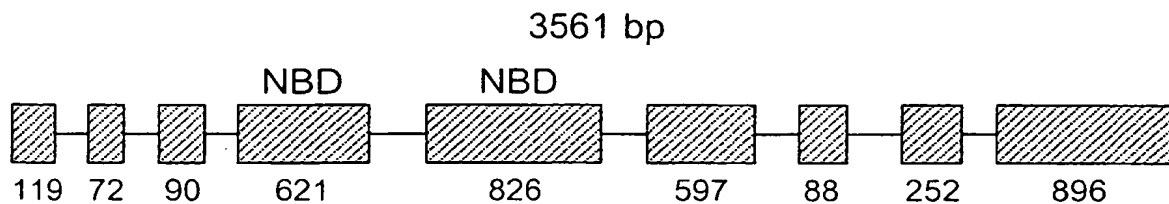
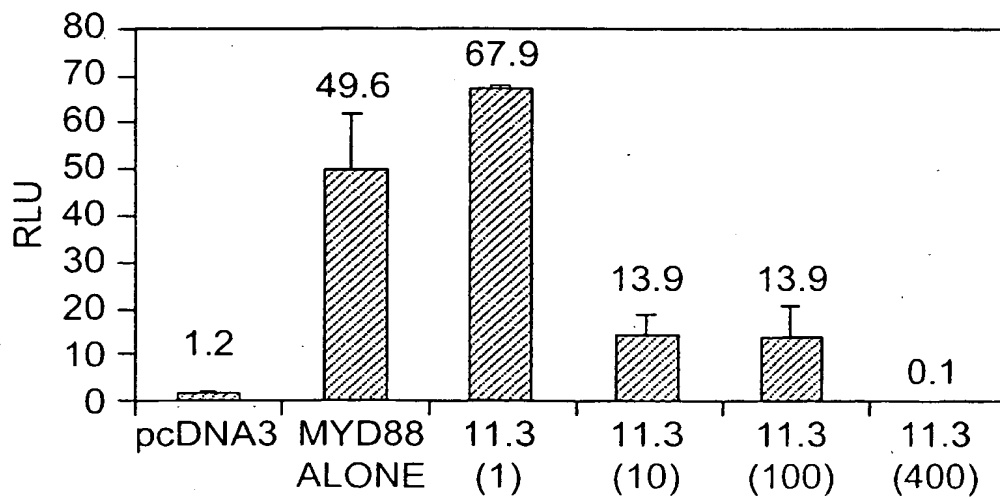


FIG. 26



11.3 TRANSFECTIONS (ng/ml)

FIG. 27
40/68

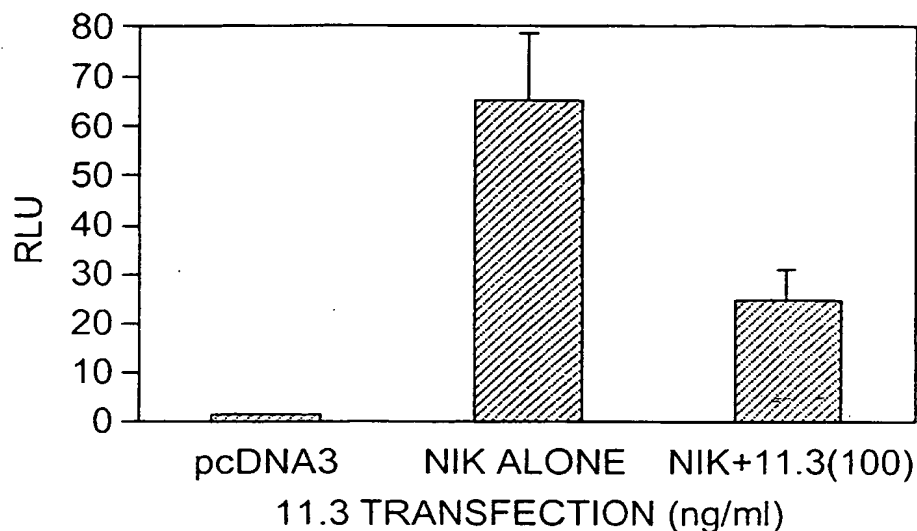


FIG. 28

```

1  ATGCTGCAGAATTTTAAGTACCCAAAGTTTCTCAACAAGTTGATTTTCAA
51  GCAAGCTCACCGGTTCCCCAGCTCATCTTCCTTCCAGTTCCCCTGTCCCC
101 CAGCTCAACTGCCTGCCCTCAGTTCACCTGTCCCCCAGTTCATCTTCCTC
151 CTAGCTCCCCTGTCCCCTAGCTCACCTGTGCCCCAGCTCCCCTGTCCCCC
201 AGGCTGGCTCCTCATGGACCCCGTTGGCCTCCAGCTCGGCAACAAGAACC
251 TGTGGAGCTGTCTTGTGAGGCTGCTCACCAAAGACCCAGAATGGCTGAAC
301 GCCAAGATGAAGTTCTTCCTCCCCAACACGGACCTGGATTCCAGGAACGA
351 GACCTTGGACCCTGAACAGAGAGTCATCCTGCAACTCAACAAGCTGCATG
401 TCCAGGGTTCGGACACCTGGCAGTCTTTCATTCAATTGTGTGTGCATGCAG
451 CTGGAGGTGCCTCTGGACCTGGAGGTGCTGCTGCTGAGTACTTTTGGCTA
501 TGATGATGGGTTCACCAGCCAGCTGGGAGCTGAGGGGAAAAGCCAACCTG
551 AATCTCAGCTCCACCATGGCCTGAAGCGCCACATCAGAGCTGTGGGTCC
601 TCACCCCGCCGGAAGCAGTGCAAGAAGCAGCAGCTAGAGTTGGCCAAGAA
651 GTACCTGCAGCTCCTGCGGACCTCTGCCCAGCAGCGCTACAGGAGCCAAA
701 TCCCTGGGTCAAGGCAGCCCCACGCCTTCCACCAGGTCTATGTCCCTCCA
751 ATCCTGCGCCGGGCCACAGCATCCTTAGACACTCCGGAGGGGGGCCATTAT
801 GGGGGACGTCAAGGTGGAAGATGCTGCTGACGTGAGCATCTCGGACCTCT

```

FIG. 29A
41/68

851 TCAACACCAGGGTTAACAAGGGCCCGAGGGTGACCGTGCTTTTGGGGAAG
901 GCTGGCATGGGCAAGACCACGCTGGCCACCGGCTCTGCCAGAAGTGGGC
951 AGAGGGCCATCTGAACTGTTTCCAGGCCCTGTTCTTTTGAATTCCGCC
1001 AGCTCAACTTGATCACGAGGTTCTTGACACCGTCCGAGCTCCTTTTTGAT
1051 CTGTACCTGAGCCCTGAATCGGACCACGACACTGTCTTCAGTACCTGGA
1101 GAAGAACGCTGACCAAGTCCTGCTGATCTTTGATGGGCTAGATGAGGCCC
1151 TCCAGCCTATGGGTCTGATGGCCCAGGCCCAGTCCTCACCTTTTCTCC
1201 CATCTCTGCAATGGGACCCTCCTGCCTGGCTGCCGGGCAGCCATGGTCCA
1251 CATGTTGGGCTTTGATGGGGCCACGGGTGGAAGAATATGTGAATCACTTCT
1301 TCAGCGCCCAGCCATCGCGGGAGGGGGCCCTGGTGGAGTTACAGACAAAT
1351 GGACGTCTCCGAAGCCTGTGTGCGGTGCCCGCACTGTGCCAAGTCGCCTG
1401 TCTCTGCCTCCACCATCTGCTTCCTGACCACGCCCCAGGCCAGTCTGTGG
1451 CCCTCCTGCCCAACATGACTCAGTCTCTATATGCAGATGGTGTCTCGCCCTC
1501 AGCCCCCTGGGCACCTGCCCCACCTCGTCCCTACTGGACCTGGGGGAGGT
1551 GGCCCTGAGGGGGCCCTGGAGACAGGGAAGGCCCTGGGCACAGCAGACAG
1601 GCTATGCTTTACCCACCTCAGCCTGCAGGAGTTTCTTGCTGCCCTGCAC
1651 CTGATGGCCAGCCCCAAGGTGAACAAAGACACACTTACCCAGTATGTTAC
1701 CCTCCATTCCCGCTGGGTACAGCGGACCAAAGCTAGACTGGGCCTCTCAG
1751 ACCACCTCCCCACCTTCCTGGCGGGCCTGGCATCCTGCACTGCGCCCC
1801 TTCCTTAGCCACCTGGCGCAGGGCAATGAGGACTGTGTGGGTGCCAAGCA
1851 GGCTGCTGTAGTGCAGGTGTTGAAGAAGTTGGCCACCCGCAAGCTCACAG
1901 GGCCAAAGGTTGTAGAGCTGTGTCACTGTGTGGATGAGACACAGGAGCCT
1951 GAGCTGGCCAGTCTCACCGCACAAAGCCTCCCCTATCAACTGCCCTTCCA
2001 CAATTTCCCACTGACCTGCACCGACCTGGCCACCCTGACCAACATCCTAG
2051 AGCACAGGGAGGCCCCCATCCACCTGGATTTTGATGGCTGTCCCCTGGAG
2101 CCCCCTGCCCCTGAGGCTCTGGTAGGCTGTGGGCAGATAGAGAATCTCAG
2151 CTTTAAGAGCAGGAAGTGTGGGGATGCCTTTGCAGAAGCCCTCTCCAGGA
2201 CTTGCGGACAATGGGGAGGCTGCAGATGCTGGGGTTAGCAGGAAGTAAA
2251 ATCACTGCCCCGAGGCATCAGCCACCTGGTGAAAGCTTTGCCTCTCTGTCC
2301 ACAGCTGAAAGAAGTCAGTTTTTCGGGACAACCAGCTCAGTGACCAAGTGG
2351 TGCTGAACATTGTGGAGGTTCTCCCTCACCTACCACGGCTCCGGAAGCTT
2401 GACCTCTCAGGGAACCAGCTGGAAGATGAAGGCTGTCCGGCTGATGGCAGA
2451 GGCTGCATCCCAGCTGCACATCGCCAGGAAGCTGGACCTCAGTAACAACG
2501 GGCTTTCTGTGGCCGGGGTGCATTGTGTGCTGAGGGCCGTGAGTGCCTGC
2551 TGGACCCTGGCAGAGCTGCACATCAGGCTGACACATTGTGGCCTCCAAGA
2601 AAAGCACCTAGAGCAGCTCTGCAAGGCTCTGGGAGGAAGCTGCCACCTCG
2651 GTCACCTCCACCTCGACTTCTCAGGCAATGCTCTGGGGGATGAAGGTGCA
2701 GCCCCGGCTGGCTCAGCTGCTCCAGGGCTGGGAGCTCTGCAGTCTTGAA
2751 CCTCAGTGAGAACGGTTTGTCCCTGGATGCCGTGTTGGGTTTGGTTCGGT
2801 GCTTCTCCACTCTGCAGTGGCTCTTCCGCTTGACATCAGCCTCAGTGAG
2851 TGTCTCTGGAGCCCCCAAGCCTCACCCGCCTCTGTGCCACTCTGAAGGA
2901 CTGCCCCGGACCCCTGGAATGCAATTGTCTGTGAGTTCTTGAGTGACC
2951 AGAGCCTGGAGACTCTACTGGACTGCTTACCTCAACTCCCTCAGCTGAGC
3001 CTGCTGCAGCTGAGCCAGACGGGACTGTCCCCGAAAAGCCCCCTTCTGCT
3051 GGCCAACACCTTAAGCCTGTGTCCACGGGTTAAAAAGGTGGATCTCAGGT
3101 TCACAGGCTGCAGCCTCAGCCAGGAGCACGTAGAGTCACTCTGCTGGTTG
3151 CTGAGCAAGTGTAAGACCTCAGCCAGGTGGATCTCTCAGCAAACCTGCT
3201 GGGCGACAGCGGACTCAGATGCCTTCTGGAATGTCTGCCGCAGGTGCCCA
3251 TCTCCGGTTTGCTTGAGAGCTTGGTCAACGGCCTGTGGGACTGTGTGCGCG
3301 ATCGCGCCCGCAACCCCAATGGCCACCGAAGTGTGCCATCCGCGTGCG
3351 ATGGGGGACACCGTGCTGCGGGCTGTCTTCAGGACATCTTATGTGGGGT
3401 ATTGCGGCGCCAATACCCGGTCACCCCTATTGCAGGGGGGGATATGGCAT
3451 TCTCCTCTATGTGG (SEQ ID NO:21)

1 MLQNFKYPKFLNKLIFKQAHFRFPSSSSFQFPCPPAQLPALSSPVPQFIFL
51 LAPLSPSSPVPQLPCPPGWLMDPVGLQLGNKNLWSCLVRLLTKDPEWLN
101 AKMKFFLPNTDLDSRNETLDPEQRVILQLNKLHVQGSWTQSFHCVCMQ
151 LEVPLDLEVLLLSTFGYDDGFTSQLGAEGKSQPESQLHHGLKRPHQSCGS
201 SPRRKQCKKQLELAKKYLQLLRTSAQQRYRSQIPGSGQPHAFHQVYVPP
251 ILRRATASLDTPEGAIMGDVKVEDGADVSI SDFNTRVNVKGRVTVLLGK
301 AGMGKTTLAHRLCQKWAEGHLNCFQALFLFEFRQLNLITRFLTPSELLFD
351 LYLSPESDHDTVFOYLEKNADQVLLIFDGLDEALQPMGPDGPGPVLTLFS
401 HLCNGTLLPGCRAAMVHMLGFDGPRVEEYVNHFFSAQPSREGALVELQTN
451 GRLRSLCAVPALCQVACLCLHHLLPDHAPGQSVALLPNMTQLYMQMVLAL
501 SPPGHLPTSSLDDLGEVALRGPGRGREGPGHQQTGYAFTHLSLQEFALALH
551 LMASPKVNKDTLTQYVTLHSRWVQRTKARLGLSDHLPFTFLAGLASCTCRP
601 FLSHLAQGNEDCVGAKQAAVVQVLKKLATRKLTPGVVVELCHCVDDETQEP
651 ELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPIHLDFDGCPL
701 PHCPEALVGCQIENLSFKSRKCGDAFAEALSRSPLTMGRQLQMLGLAGSK
751 ITARGISHLVKALPLCPQLKEVSFRDNQLSDQVVLNIVEVLPPLRLRKL
801 DLSGNQLEDEGCRLMAEAAASQLHIARKLDLSNNGLSVAGVHCVLRAVSAC
851 WTLAELHIRLTHCGLEKHEQLCKALGGSCHLGHLHLDFSGNALGDEGA
901 ARLAQLLPGLGALQSLNLSENGLSLDAVLGLVRCFSTLQWLFRDLISLSE
951 CPLEPPSLTRLCATLKDCPGPLELQLSCEFLSDQSLETLLDCLPQLPQLS
1001 LLQLSQTGLSPKSPFLLANTLSLCPRVKVVDLRFTGCSLSQEHVESLCWL
1051 LSKCKDLSQVDLSANLLGDSGLRCLLECLPQVPI SGLLESILTACGTVSP
1101 IAPGNPQWPPKCAIRVRWGTGCCGLSFRTSYVGYCGANTRSPLLQGGIWH
1151 SPLC (SEQ ID NO:22)

FIG. 29C

1 GGCCAGTCCTCACCCCTTTTCTCCCATCTCTGCAATGGGACCCTCCTGCC
51 TGGCTGCCGGGTGATGGCTACCTCCCGTCCAGGGAAGCTGCCTGCCTGCC
101 TGCCTGCAGAGGCAGCCATGGTCCACATGTTGGGCTTTGATGGGCCACGG
151 GTGGAAGAATATGTGAATCACTTCTTCAGCGCCCAGCCATCGCGGGAGGG
201 GGCCCTGGTGGAGTTACAGACAAATGGACGTCTCCGAAGCCTGTGTGCGG
251 TGCCCGCACTGTGCCAAGTCGCCTGTCTCTGCCTCCACCATCTGCTTCCT
301 GACCACGCCCCAGGCCAGTCTGTGGCCCTCCTGCCCAACATGACTCAGCT
351 CTATATGCAGATGGTGCTCGCCCTCAGCCCCCCTGGGCACTTGCTCACCT
401 CGTCCCTACTGGACCTGGGGGAGGTGGCCCTGAGGGGCCTGGAGACAGGG
451 AAGGTTATCTTCTATGCAAAGATATTGCTCCACCCTTGATAGCTTTTGG
501 GGCCACTCACAGCCTGCTGACTTCTTCTGCGTCCGCACAGGCCCTGGGC
551 ACCAGCAGACAGGCTATGCTTTTACCCACCTCAGCCTGCAGGAGTTTCTT
601 GCTGCCCTGCACCTGATGGCCAGCCCCAAGGTGAACAAAGACACACTTAC
651 CCAGTATGTTACCCTCCATTCCCGCTGGGTACAGCGGACCAAAGCTAGAC
701 TGGGCCTCTCAGACCACCTCCCCACCTTCTTGGCGGGCCTGGCATCTGC
751 ACCTGCCGCCCCCTTCTTAGCCACCTGGCGCAGGGCAATGAGGACTGTGT
801 GGGTGCCAAGCAGGCTGCTGTAGTGACAGGTGTTGAAGAAGTTGGCCACCC
851 GCAAGCTCACAGGGCCAAAGGTTGTAGAGCTGTGTCACTGTGTGGATGAG
901 ACACAGGAGCCTGAGCTGGCCAGTCTCACCGCACAAAGCCTCCCCTATCA
951 ACTGCCCTTCCACAATTTCCCAGTACCTGCACCGACCTGGCCACCCTGA
1001 CCAACATCCTAGAGCACAGGGAGGCCCCATCCACCTGGATTTTGTATGGC
1051 TGTCCCCTGGAGCCCCCACTGCCCTGAGGCTCTGGTAGGCTGTGGGCAGAT
1101 AGAGAATCTCAGCTTTAAGAGCAGGAAGTGTGGGGATGCCTTTGAGAGAG
1151 CCCTCTCCAGGAGCTTGCCGACAATGGGGAGGCTGCAGATGCTGGGGTTA

FIG. 29D

1201 GCAGGAAGTAAAATCACTGCCCCGAGGCATCAGCCACCTGGTGAAAGCTTT
1251 GCCTCTCTGTCCACAGCTGAAAGAAGTCAGTTTTTCGGGACAACCAGCTCA
1301 GTGACCAGGTGGTGCTGAACATTGTGGAGGTTCTCCCTCACCTACCACGG
1351 CTCCGGAAGCTTGACCTGAGCAGCAACAGCATCTGCGTGTCAACCCTACT
1401 CTGCTTGGCAAGGGTGGCAGTCACGTGTCTTACCGTCAGGATGCTTCAGG
1451 CCAGGGAGCGGACCATCATCTTCTTCTTCCCCGCCACAGAGACAACCT
1501 GCAGAGCTACAAAGAGCTCCAGACCTGCAGGAAAGTGACGGCCAGAGGAA
1551 AGGGGCTCAGAGCAGAAGCTTGACGCTCAGGCTGCAGAAGTGTGAGCTCC
1601 AGGTCCACGATGCGGAGGCCCTCATAGCCCTGCTCCAGGAAGGCCCTCAC
1651 CTGGAGGAAGTGGACCTCTCAGGGAACCAGCTGGAAGATGAAGGCTGTGCG
1701 GCTGATGGCAGAGGCTGCATCCCAGCTGCACATCGCCAGGAAGCTGGACC
1751 TCAGCGACAACGGGGCTTTCTGTGGCCGGGGTGCATTGTGTGCTGAGGGCC
1801 GTGAGTGCGTGCTGGACCCTGGCAGAGCTGCACATCAGCCTGCAGCACAA
1851 AACTGTGATCTTCATGTTTGCCCAGGAGCCAGAGGAGCAGAAGGGGCCCC
1901 AGGAGAGGGCTGCATTTCTTGACAGCCTCATGCTCCAGATGCCCTCTGAG
1951 CTGCCTCTGAGCTCCCGAAGGATGAGGCTGACACATTGTGGCCTCCAAGA
2001 AAAGCACCTAGAGCAGCTCTGCAAGGCTCTGGGAGGAAGCTGCCACCTCG
2051 GTCACCTCCACCTCGACTTCTCAGGCAATGCTCTGGGGGATGAAGGTGCA
2101 GCCCCGGCTGGCTCAGCTGCTCCAGGGCTGGGAGCTCTGCAGTCCTTGAA
2151 CCTCAGTGAGAACGGTTTGTCCCTGGATGCCGTGTTGGGCTTGTTTCGGT
2201 GCTTCTCCACTCTGAGTGGCTCTTCCGCTTGACATCAGCTTTGAAAGC
2251 CAACACATCCTCCTGAGAGGGGACAAAGACAAGCAGCCTCAGTGAGTGTCTC
2301 TCTGGAGCCCCCAAGCCTCACCCGCCTCTGTGCCACTCTGAAGGACTGCC
2351 CGGGACCCCTGGAAGTGAATTGTCTGTGAGTTCCTGAGTGACCAGAGC
2401 CTGGAGACTCTACTGGACTGCTTACCTCAACTCCCTCAGCTGAGCCTGCT
2451 GCAGCTGAGCCAGACGGGACTGTCCCCGAAAAGCCCTTCTGCTGGCCA
2501 ACACCTTAAGCCTGTGTCCACGGGTAAAAAGGTGGATCTCAGGTCCCTG
2551 CACCATGCAACTTTGCACTTCAGATCCAACGAGGAGGAGGAAGGCGTGTG
2601 CTGTGGCAGGTTACAGGCTGCAGCCTCAGCCAGGAGCACGTAGAGTCAC
2651 TCTGCTGGTTGCTGAGCAAGTGTAAGACCTCAGCCAGGTGGATCTGAGT
2701 CACAACAGCATTTCTCAGGAAAGTGCCCTGTACCTGCTGGAGACACTGCC
2751 CTCCTGCCCACGTGTCCGGGAGGCCTCAGTGAACCTGGGCTCTGAGCAGA
2801 GCTTCCGGATTCACTTCTCCAGAGAGGACCAGGCTGGGAAGACACTCAGG
2851 CTAAGTGAGTGCAGCTTCCGGCCAGAGCACGTGTCCAGGCTGGCCACCGG
2901 CTTGAGCAAGTCCCTGCAGCTGACGGAGCTCACGCTGACCCAGTGCTGCC
2951 TGGGCCAGAAGCAGCTGGCCATCCTCCTGAGCTTGGTGGGGCGACCCGCA
3001 GGGCTGTTTCAGCCTCAGGGTGCAGGAGCCGTGGGCGGACAGAGCCAGGGT
3051 TCTCTCCCTGTTAGAAGTCTGCGCCAGGCCTCAGGCAGTGTCACTGAAA
3101 TCAGCATCTCCGAGACCCAGCAGCAGCTCTGTGTCCAGCTGGAATTTCTT
3151 CGCCAGGAAGAGAATCCAGAAGCTGTGGCACTCAGGTTGGCTCACTGTGA
3201 CCTTGGAGCCCACCACAGCCTTCTTGTGCGGCAGCTGATGGAGACATGTG
3251 CCAGGCTGCAGCAGCTCAGCTTGTCTCAGGTTAACCTCTGTGAGGACGAT
3301 GATGCCAGTTCCTGCTGCTGCAGAGCCTCCTGCTGTCCCTCTCTGAGCT
3351 GAAGACATTTTCGGCTGACCTCCAGCTGTGTGAGCACCGAGGGCCTCGCCC
3401 ACCTGGCATCTGGTCTGGGCCACTGCCACCACTTGGAGGAGCTGGACTTG
3451 TCTAACAATCAATTTGATGAGGAGGGCACCAAGGCGCTGATGAGGGCCCT
3501 TGAGGGGAAATGGATGCTAAGAGGGCTGGACCTCAGTACCTTCTGCTGA
3551 AGAGCTCCACCTTGGCCTTGCTTACTACAGACTAAGCCAGATGACCTGC
3601 CTGCAGAGCCTCAGACTGAACAGGAACAGTATCGGTGATGTCGGTTGCTG
3651 CCACCTTTCTGAGGCTCTCAGGGCTGCCACCAGCCTAGAGGAGCTGGACT
3701 TGAGCCACAACCAGATTGGAGACGCTGGTGTCCAGCACTTAGCTACCATC

Rec'd PCT/PTO 21 OCT 2004

3751 CTGCCTGGGCTGCCAGAGCTCAGGAAGATAGACCTCTCAGGGAATAGCAT
3801 CAGCTCAGCCGGGGGAGTGCAGTTGGCAGAGTCTCTCGTTCTTTGCAGGC
3851 GCCTGGAGGAGTTGATGCTTGGCTGCAATGCCCTGGGGGATCCCACAGCC
3901 CTGGGGCTGGCTCAGGAGCTGCCCCAGCACCTGAGGGTCTTACACCTACC
3951 ATTCAGCCATCTGGGCCCAGGTGGGGCCCTGAGCCTGGCCCAGGCCCTGG
4001 ATGGATCCCCCATTTGGAAGAGATCAGCTTGGCGGAAAACAACCTGGCT
4051 GGAGGGGTCTGCGTTTCTGTATGGAGCTCCCGCTGCTCAGACAGATAGA
4101 CCTGGTTTCTGTAAAGATTGACAACCAGACTGCCAAGCTCCTCACCTCCA
4151 GCTTCACGAGCTGCCCTGCCCTGGAAGTAATCTTGCTGTCCTGGAATCTC
4201 CTCGGGGATGAGGCAGCTGCCGAGCTGGCCCAGGTGCTGCCGAAGATGGG
4251 CCGGCTGAAGAGAGTGGACCTGGAGAAGAATCAGATCACAGCTTTGGGGG
4301 CCTGGCTCCTGGCTGAAGGACTGGCCCAGGGGTCTAGCATCCAAGTCATC
4351 CGCCTCTGGAATAACCCCATTCCTGCGACATGGCCCAGCACCTGAAGAG
4401 CCAGGAGCCCAGGCTGGACTTTGCCTTCTTTGACAACCAGCCCCAGGCC
4551 CTTGGGGTACTTGA (SEQ ID NO:23)

FIG. 29F

1 GPVLTFLFSLCNGTLLPGCRVMATSRPGKLPACLPAEAAMVHMLGFDGPR
51 VEEYVNHFFSAQPSREGALVELQTNGLRSLCAVPALCQVACLCLHLLP
101 DHAPGQSVALLPNMTQLYMQMVLALSPPGHLLTSSLLDLGEVALRGLETG
151 KVIFYAKDIAPPLIAFGATHSLTTSFRVCTGPGHQQTGYAFTHLSLQEF
201 AALHLMASPKVNKDTLTQYVTLHSRWVQRTKARLGLSDHLPTFLAGLASC
251 TCRPFLSHLAQGNEDCVGAKQAAVVQVLKKLATRKLTPGVVELCHCVDE
301 TQPELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPIHLDFDG
351 CPLEPHCPEALVGCGQIENLSFKSRKCGDAFAEALSRLPTMGRLQMLGL
401 AGSKITARGISHLVKALPLCPQLKEVSFRDNQLSDQVVLNIVEVLPPLPR
451 LRKLDLSSNSICVSTLLCLARVAVTCTVRMLQARERTIIIFLLSPPTETT
501 AELQRAPDLQESDGQRKGAQSRSLTLRLQKQQLQVHDAEALIALLOEGPH
551 LEEVDLSGNQLEDEGCRLMAEASQLHIARKLDLSDNGLSVAGVHCVLRA
601 VSACWTLAELHISLQHKTVIFMFAQEPEEQKGPQERAAFLDSLMLQMPSE
651 LPLSSRRMRLTHCGLQEKHLEQLCKALGGSCHLGHLLHDFSGNALGDEGA
701 ARLAQLLPGLGALQSLNLSENGLSLDAVLGLVRCFSTLQWLFRLDISFES
751 QHILLRGDKTSSLSECPLEPPSLTRLCATLKDCPGPLELQLSCEFLSDQS
801 LETLLDCLPQLPQLSLLQLSQTGLSPKSPFLLANTLSLCPRVKKVDLRSL
851 HHATLHFRSNEEEEGVCCGRFTGCSLSQEHVESLCWLLSKCKDLSQVDLS
901 HNSISQESALYLLETLPSCPRVREASVNLGSEQSFRIHFSREDQAGKTLR
951 LSECSFRPEHVSRLATGLSKSLQLTELTLTQCCLGQKQLAILLSLVGRPA
1001 GLFSLRVQEPWADRARVLSLLEVCAQASGSVTEISISSETQQQLCVQLEFP
1051 RQEENPEAVALRLAHCDLGAHHSLLVGQLMETCARLQQLSLSQVNLCEDD
1101 DASSLLLQSLLLSLSELKTFRLTSSCVSTEGLAHLASGLGHCHHLEELDL
1151 SNNQFDEEGTKALMRALEGKWMKRLDLSHLLNSSTLALLTHRLSQMTC
1201 LQSLRLNRNSIGDVGCHLSEALRAATSLEELDLSHNQIGDAGVQHLATI
1251 LPGLPELRKIDLSGNSISSAGGVQLAESLVLCCRLEELMLGCNALGDPTA
1301 LGLAQELPQHLRVLHLPFSLHLPGGALSQAQALDGSPLHEEISLAENNL
1351 GGVLRFCMELPLLRQIDLVSCKIDNQITAKLLTSSFTSCPALÉVILLSWNL
1401 LGDEAAAELAQVLPKMGRLLKRVLDLEKNQITAGAWLLAEGLAQGSSIQVI
1451 RLWNNPIPCDMAQHLKSQEPRLDFAFFDNQPQAPWGT
(SEQ ID NO:24)

FIG. 29G

1 ATGGACCCCGTTGGCCTCCAGCTCGGCAACAAGAACCTGTGGAGCTGTCTTGTGAGGCTG
1 M D P V G L Q L G N K N L W S C L V R L
61 CTCACCAAAGACCCAGAATGGCTGAACGCCAAGATGAAGTTCTTCCCTCCCAACACGGAC
21 L T K D P E W L N A K M K F F L P N T D
121 CTGGATTCCAGGAACGAGACCTTGGACCCTGAACAGAGAGTCATCCTGCAACTCAACAAG
41 L D S R N E T L D P E Q R V I L Q L N K
181 CTGCATGTCCAGGGTTCGGACACCTGGCAGTCTTTCATTTCATTGCGTGTGCATGCAGCTG
61 L H V Q G S D T W Q S F I H C V C M Q L
241 GAGGTGCCTCTGGACCTGGAGGTGCTTCTGCTAAGTACTTTTGGCTATGATGATGGGTTC
81 E V P L D L E V L L L S T F G Y D D G F
301 ACCAGCCAGCTGGGAGCTGAGGGGAAAAGCCAACCTGAATCTCAGCTCCACCATGGCCTG
101 T S Q L G A E G K S Q P E S Q L H H G L
361 AAGCGCCACATCAGAGCTGTGGGTCTCACCCCGCGGAAGCAGTGAAGAAGCAGCAG
121 K R P H Q S C G S S P R R K Q C K K Q Q
421 CTAGAGTTGGCCAAGAAGTACCTGCAGCTCCTGCGGACCTCTGCCAGCAGCGCTACAGG
141 L E L A K K Y L Q L L R T S A Q Q R Y R
481 AGCCAAATCCCTGGGTGAGGGCAGCCCCACGCCTTCCACCAGGTCTATGTCCCTCCAATC
161 S Q I P G S G Q P H A F H Q V Y V P P I
541 CTGCGCCGGGCCACAGCATCCTTAGACACTCCGGAGGGGGCCATATAGGGGGACGTCAAG
181 L R R A T A S L D T P E G A I M G D V K
601 GTGGAAGATGGTGCTGACGTGAGCATCTCGGACCTCTTCAACACCAGGGTTAACAAGGGC
201 V E D G A D V S I S D L F N T R V N K G
661 CCGAGGGTGACCGTGCTTTTGGGGAAGGCTGGCATGGGCAAGACCACGCTGGCCCCACCGG
221 P R V T V L L G K A G M G K T T L A H R
721 CTCTGCCAGAAGTGGGCAGAGGGCCATCTGAACTGTTTCCAGGCCCTGTTCTTTTGTAA
241 L C Q K W A E G H L N C F Q A L F L F E
781 TTCCGCCAGCTCAACTTGATCACGAGGTTCCTGACACCGTCCGAGCTCCTTTTTGATCTG
261 F R Q L N L I T R F L T P S E L L F D L
841 TACCTGAGCCCTGAATCGGACCACGACTGTCTTCCAGTACCTGGAGAAGAACGCTGAC
281 Y L S P E S D H D T V F Q Y L E K N A D
901 CAAGTCTGTGATCTTTGATGGGCTAGATGAGGCCCTCCAGCCTATGGGTCTGTATGGC
301 Q V L L I F D G L D E A L Q P M G P D G
961 CCAGGCCAGTCTCACCCTTTTCTCCCATCTCTGCAATGGGACCCTCCTGCCTGGCTGC
321 P G P V L T L F S H L C N G T L L P G C
1021 CGGGTGATGGCTACCTCCCGTCCAGGGAAGCTGCCTGCCTGCCTGCCTGCAGAGGCAGCC
341 R V M A T S R P G K L P A C L P A E A A
1081 ATGGTCCACATGTTGGGCTTTGATGGGCCACGGGTGGAAGAATATGTGAATCACTTCTTC
361 M V H M L G F D G P R V E E Y V N H F F
1141 AGCGCCAGCCATCGCGGGAGGGGGCCCTGGTGGAGTTACAGACAAATGGACGTCTCCGA
381 S A Q P S R E G A L V E L Q T N G R L R
1201 AGCCTGTGTGCGGTGCCGCACTGTGCAAGTCGCTGTCTGTGCTCCACCATCTGCTT
401 S L C A V P A L C Q V A C L C L H H L L
1261 CCTGACCACGCCCCAGGCCAGTCTGTGGCCCTCCTGCCCAACATGACTCAGCTCTATATG
421 P D H A P G Q S V A L L P N M T Q L Y M
1321 CAGATGGTGCTCGCCCTCAGCCCCCTGGGCACTTGCCACCTCGTCCCTACTGGACCTG
441 Q M V L A L S P P G H L P T S S L L D L
1381 GGGGAGGTGGCCCTGAGGGGCTGGAGACAGGGAAGGTTATCTTCTATGCAAAAGATATT
461 G E V A L R G L E T G K V I F Y A K D I
1441 GCTCCACCCTTGATAGCTTTTGGGGCCACTCACAGCCTGCTGACTTCTTCTGCGTCTGC
481 A P P L I A F G A T H S L L T S F C V C
1501 ACAGGCCCTGGGCACCAGCAGACAGGCTATGCTTTCACCCACCTCAGCCTGCAGGAGTTT
501 T G P G H Q Q T G Y A F T H L S L Q E F
1561 CTTGCTGCCCTGCACCTGATGGCCAGCCCCAAGGTGAACAAAGACACACTTACCCAGTAT
521 L A A L H L M A S P K V N K D T L T Q Y

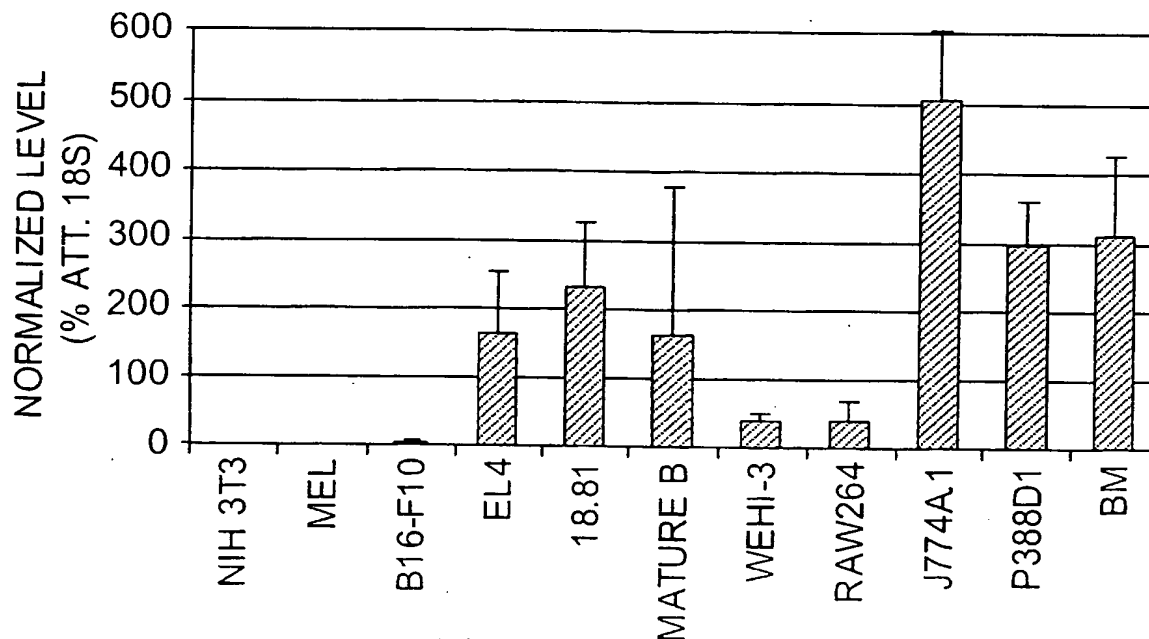
1621 GTTACCCTCCATTCCCCTGGGTACAGCGGACCAAGCTAGACTGGGCCTCTCAGACCAC
541 V T L H S R W V Q R T K A R L G L S D H
1681 CTCCCCACCTTCTGGCGGGCTGGCATCTGCACCTGCCGCCCTTCCTTAGCCACCTG
561 L P T F L A G L A S C T C R P F L S H L
1741 GCGCAGGGCAATGAGGACTGTGTGGGTGCCAAGCAGGCTGCTGTAGTGCAGGTGTTGAAG
581 A Q G N E D C V G A K Q A A V V Q V L K
1801 AAGTTGGCCACCCGCAAGCTCACAGGGCCAAAGGTTGTAGAGCTGTGTCACTGTGTGGAT
601 K L A T R K L T G P K V V E L C H C V D
1861 GAGACACAGGAGCCTGAGCTGGCCAGTCTCACCGCACAAAGCCTCCCCTATCAACTGCCC
621 E T Q E P E L A S L T A Q S L P Y Q L P
1921 TTCCACAATTTCCCACTGACCTGACCCGAGCTGGCCACCTGACCAACATCTAGAGCAC
641 F H N F P L T C T D L A T L T N I L E H
1981 AGGGAGGCCCCCATCCACCTGGATTTTGATGGCTGTCCCCTGGAGCCCCACTGCCCTGAG
681 R E A P I H L D F D G C P L E P H C P E
2041 GCTCTGGTAGGCTGTGGGCAGATAGAGAATCTCAGCTTTAAGAGCAGGAAGTGTGGGGAT
701 A L V G C G Q I E N L S F K S R K C G D
2101 GCCTTTGCAGAAGCCCTCTCCAGGAGCTTGCCGACAATGGGGAGGCTGCAGATGCTGGGG
721 A F A E A A L S R S L P T M G R L Q M L G
2161 TTAGCAGGAAGTAAATCACTGCCGAGGCATCAGCCACCTGGTGAAAGCTTTGCCTCTC
741 L A G S K I T A R G I S H L V K A L P L
2221 TGTCCACAGCTGAAAGAAGTCAGTTTTCGGGACAACCAGCTCAGTGACCAGGTGTGCTG
761 C P Q L K E V S F R D N Q L S D Q V V L
2281 AACATTGTGGAGGTTCTCCCTCACCTACCACGGCTCCGGAAGCTTGACCTGAGCAGCAAC
781 N I V E V L P H L P R L R K L D L S S N
2341 AGCATCTGCGTGTCAACCCTACTCTGCTTGGCAAGGGTGGCAGTCACGTGTCCTACCGTC
801 S I C V S T L L C L A R V A V T C P T V
2401 AGGATGCTTCAGGCCAGGGAGCGGACCATCATCTTCCTTCTTTCCCCGCCCCACAGAGACA
821 R M L Q A R E R T I I F L L S P P T E T
2461 ACTGCAGAGCTACAAAGAGCTCCAGACCTGCAGGAAAGTGACGGCCAGAGGAAAGGGCT
841 T A E L Q R A P D L Q E S D G Q R K G A
2521 CAGAGCAGAAGCTTGACGCTCAGGCTGCAGAAGTGTGAGCTCCAGGTCCACGATGCGGAG
861 Q S R S L T L R L Q K C Q L Q V H D A E
2581 GCCCTCATAGCCCTGCTCCAGGAAGGCCCTCACCTGGAGGAAGTGGACCTCTCAGGGAAC
881 A L I A L L Q E G P H L E E V D L S G N
2641 CAGCTGGAAGATGAAGGCTGTGCGCTGATGGCAGAGGCTGCATCCCAGCTGCACATCGCC
901 Q L E D E G C R L M A E A A S Q L H I A
2701 AGGAAGCTGGACCTACGCGACAACGGCTTTCTGTGGCCGGGGTGCATTGTGTGCTGAGG
921 R K L D L S D N G L S V A G V H C V L R
2761 GCCGTGAGTGCGTGCTGGACCCTGGCAGAGCTGCACATCAGCCTGCAGCACAAAAGTGTG
941 A V S A C W T L A E L H I S L Q H K T V
2821 ATCTTCATGTTTGCCAGGAGCCAGAGGAGCAGAAGGGGCCCCAGGAGAGGGCTGCATTT
961 I F M F A Q E P E E Q K G P Q E R A A F
2881 CTTGACAGCCTCATGCTCCAGATGCCCTCTGAGCTGCCTCTGAGCTCCCCAAGGATGAGG
981 L D S L M L Q M P S E L P L S S R R M R
2941 CTGACACATTGTGGCCTCCAAGAAAAGCACCTAGAGCAGCTCTGCAAGGCTCTGGGAGGA
1001 L T H C G L Q E K H L E Q L C K A L G G
3001 AGCTGCCACCTCGGTACCTCCACCTCGACTTCTCAGGCAATGCTCTGGGGGATGAAGGT
1021 S C H L G H L H L D F S G N A L G D E G
3061 GCAGCCCGGCTGGCTCAGCTGCTCCCAGGGCTGGGAGCTCTGCAGTCCTTGAACCTCAGT
1041 A A R L A Q L L P G L G A L Q S L N L S
3121 GAGAACGGTTTGTCCTGGATGCCGTGTTGGGCTTGGTTCCGGTGCTTCTCCACTCTGCAG
1061 E N G L S L D A V L G L V R C F S T L Q
3181 TGGCTCTTCCGCTTGGACATCAGCTTTGAAAGCCAACACATCCTCCTGAGAGGGGACAAG
1081 W L F R L D I S F E S Q H I L L R G D K

Rec'd PCT/PTO 21 OCT 2004

3241 ACAAGCAGGGATATGTGGGCCACTGGATCTTTGCCAGACTTCCCAGCTGCAGCCAAGTTC
2001 T S R D M W A T G S L P D F P A A A K F
3301 TTAGGGTTCCGTCAGCGCTGCATCCCCAGGAGCCTCTGCCTCAGTGAGTGTCTCTGGAG
2021 L G F R Q R C I P R S L C L S E C P L E
3361 CC`CCCAAGCCTCACCCGCTCTGTGCCACTCTGAAGGACTGCCCGGGACCCCTGGAAGTCTG
2041 P P S L T R L C A T L K D C P G P L E L
3421 CAATTGTCCTGTGAGTTCCTGAGTGACCAGAGCCTGGAGACTCTACTGGACTGCTTACCT
2061 Q L S C E F L S D Q S L E T L L D C L P
3481 CAACTCCCTCAGCTGAGCCTGCTGCAGCTGAGCCAGACGGGACTGTCCCCGAAAAGCCCC
2081 Q L P Q L S L L Q L S Q T G L S P K S P
3541 TTCCTGTGGCCAACACCTTAAGCCTGTGTCCACGGGTAAAAAGGTGGATCTCAGGTCC
2101 F L L A N T L S L C P R V K K V D L R S
3601 CTGCACCATGCAACTTTGCACTTCAGATCCAACGAGGAGGAGGAAGGCGTGTGTGTGGC
2121 L H H A T L H F R S N E E E E G V C C G
3661 AGGTTACAGGCTGCAGCCTCAGCCAGGAGCACGTAGAGTCACTCTGCTGGTTGCTGAGC
2141 R F T G C S L S Q E H V E S L C W L L S
3721 AAGTGTAAGACCTCAGCCAGGTGGATCTCTCAGCAAACCTGCTGGGCGACAGCGGACTC
2161 K C K D L S Q V D L S A N L L G D S G L
3781 AGATGCCTTCTGGAATGTCTGCCGAGGTGCCCATCTCCGGTTTGCTTGATCTGAGTCAC
2181 R C L L E C L P Q V P I S G L L D L S H
3841 AACAGCATTCTCAGGAAAGTGCCCTGTACCTGCTGGAGACACTGCCCTCCTGCCACCT
2201 N S I S Q E S A L Y L L E T L P S C P R
3901 GTCCGGGAGGCCTCAGTGAACCTGGGCTCTGAGCAGAGCTTCCGGATTCACTTCTCCAGA
2221 V R E A S V N L G S E Q S F R I H F S R
3961 GAGGACCAGGCTGGGAAGACACTCAGGCTAAGTGAGTGCAGCTTCCGGCCAGAGCACGTG
2241 E D Q A G K T L R L S E C S F R P E H V
4021 TCCAGGCTGGCCACCGGCTTGAGCAAGTCCCTGCAGCTGACGGAGCTCACGCTGACCCAG
2261 S R L A T G L S K S L Q L T E L T L T Q
4081 TGCTGCCTGGGCCAGAAGCAGCTGGCCATCCTCCTGAGCTTGGTGGGCGACCCCGG
2281 C C L G Q K Q L A I L L S L V G R P A G
4141 CTGTTTCAGCCTCAGGGTGCAGGAGCCGTGGGCGGACAGAGCCAGGGTTCTCTCCCTGTTA
2301 L F S L R V Q E P W A D R A R V L S L L
4201 GAAGTCTGCGCCCAGGCCTCAGGCAGTGTCACTGAAATCAGCATCTCCGAGACCCAGCAG
2321 E V C A Q A S G S V T E I S I S E T Q Q
4261 CAGCTCTGTGTCCAGCTGGAATTTCTCGCCAGGAAGAGAATCCAGAAGCTGTGGCACTC
2341 Q L C V Q L E F P R Q E E N P E A V A L
4321 AGGTTGGCTCACTGTGACCTTGGAGCCCACCACAGCCTTCTTGTGCGGCAGCTGATGGAG
2361 R L A H C D L G A H H S L L V G Q L M E
4381 ACATGTGCCAGGCTGCAGCAGCTCAGCTTGTCTCAGGTTAACCTCTGTGAGGACGATGAT
2381 T C A R L Q Q L S L S Q V N L C E D D D
4441 GCCAGTTCCTGCTGCTGCAGAGCCTCCTGCTGTCCCTCTCTGAGCTGAAGACATTTCCG
2401 A S S L L L Q S L L L S L S E L K T F R
4501 CTGACCTCCAGCTGTGTGAGCACCGAGGGCCTCGCCACCTGGCATCTGGTCTGGGCCAC
2421 L T S S C V S T E G L A H L A S G L G H
4561 TGCCACCACTTGGAGGAGCTGGACTTGTCTAACAATCAATTTGATGAGGAGGGCACCAAG
2441 C H H L E E L D L S N N Q F D E E G T K
4621 GCGCTGATGAGGGCCCTTGAGGGGAAATGGATGCTAAAGAGGCTGGACCTCAGTCACCTT
2461 A L M R A L E G K W M L K R L D L S H L
4681 CTGCTGAACAGCTCCACCTTGGCCTTGCTTACTCACAGACTAAGCCAGATGACCTGCCTG
2481 L L N S S T L A L L T H R L S Q M T C L
4741 CAGAGCCTCAGACTGAACAGGAACAGTATCGGTGATGTGCGTTGCTGCCACCTTTCTGAG
2501 Q S L R L N R N S I G D V G C C H L S E
4801 GCTCTCAGGGCTGCCACCAGCCTAGAGGAGCTGGACTTGAGCCACAACCAGATTGGAGAC
2521 A L R A A T S L E E L D L S H N Q I G D

4861 GCTGGTGTCCAGCACTTAGCTACCATCCTGCCTGGGCTGCCAGAGCTCAGGAAGATAGAC
 2541 A G V Q H L A T I L P G L P E L R K I D
 4921 CTCTCAGGGAATAGCATCAGCTCAGCCGGGGGAGTGCAGTTGGCAGAGTCTCTCGTTCTT
 2561 L S G N S I S S A G G V Q L A E S L V L
 4981 TGCAGGCGCCTGGAGGAGTTGATGCTTGGCTGCAATGCCCTGGGGGATCCCACAGCCCTG
 2581 C R R L E E L M L G C N A L G D P T A L
 5041 GGGCTGGCTCAGGAGCTGCCCCAGCACCTGAGGGTCCTACACCTACCATTACGCCATCTG
 2601 G L A Q E L P Q H L R V L H L P F S H L
 5101 GGCCAGGTGGGGCCCTGAGCCTGGCCAGGCCCTGGATGGATCCCCCATTTGGAAGAG
 2621 G P G G A L S L A Q A L D G S P H L E E
 5161 ATCAGCTTGGCGGAAAACAACCTGGCTGGAGGGGTCCTGCGTTTCTGTATGGAGCTCCCG
 2641 I S L A E N N L A G G V L R F C M E L P
 5221 CTGCTCAGACAGATAGACCTGGTTTCTGTAAGATTGACAACCAGACTGCCAAGCTCCTC
 2661 L L R Q I D L V S C K I D N Q T A K L L
 5281 ACCTCCAGCTTCACGAGCTGCCCTGCCCTGGAAGTAATCTTGCTGTCTCTGGAATCTCCTC
 2681 T S S F T S C P A L E V I L L S W N L L
 5341 GGGGATGAGGCAGCTGCCGAGCTGGCCAGGTGCTGCCGAAGATGGGCCGGCTGAAGAGA
 2701 G D E A A A E L A Q V L P K M G R L K R
 5401 GTGGACCTGGAGAAGAATCAGATCACAGCTTTGGGGCCTGGCTCCTGGCTGAAGGACTG
 2721 V D L E K N Q I T A L G A W L L A E G L
 5464 GCCCAGGGGTCTAGCATCCAAGTCATCCGCCTCTGGAATAACCCCATTCCTGCGCATG
 2741 A Q G S S I Q V I R L W N N P I P C D M
 5521 GCCCAGCACCTGAAGAGCCAGGAGCCAGGCTGGACTTTGCCTTCTTTGACAACCAGCCC
 2761 A Q H L K S Q E P R L D F A F F D N Q P
 5581 CAGGCCCTTGGGGTACTTGA (SEQ ID NO:183)
 2781 Q A P W G T - (SEQ ID NO:184)

FIG. 30D

FIG. 31A
49/68

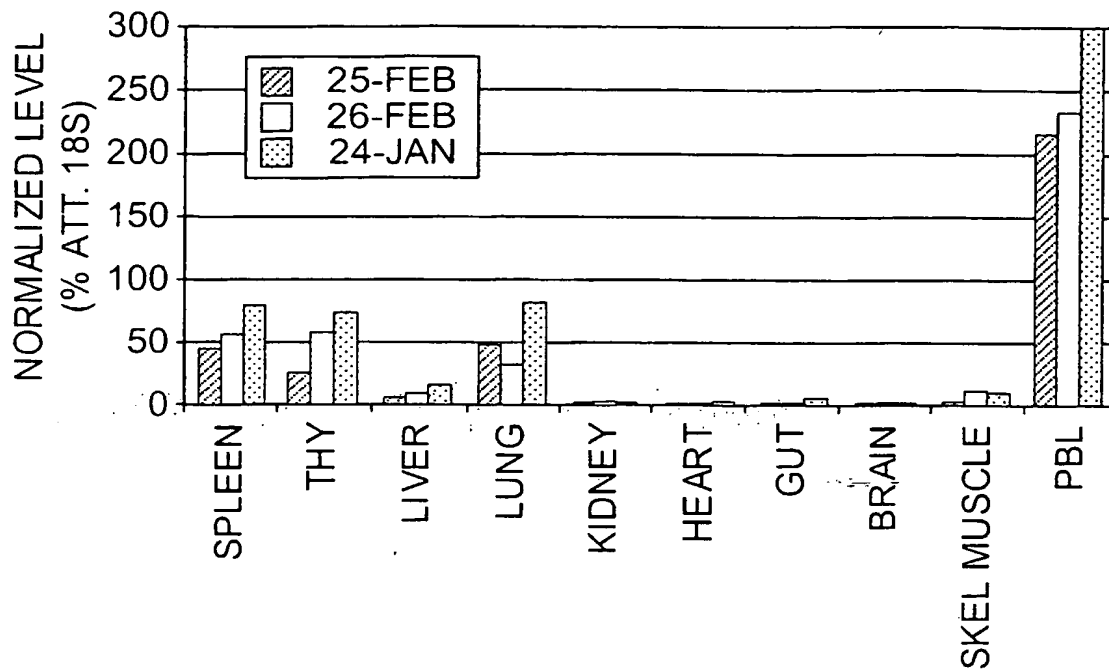


FIG. 31B

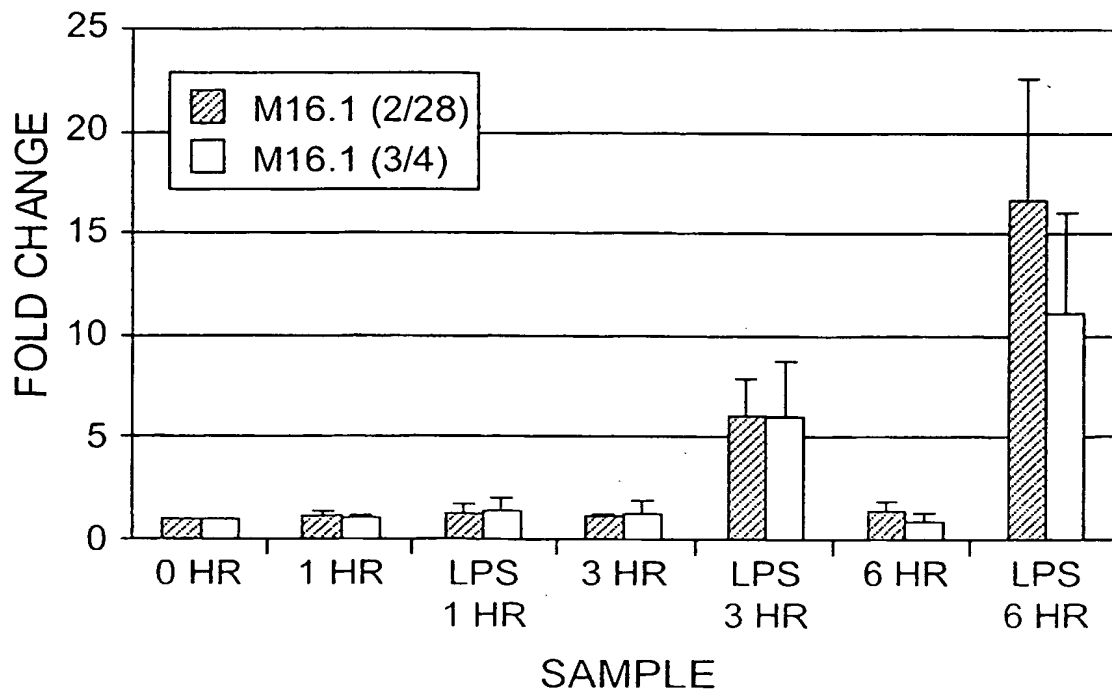


FIG. 31C
50/68

Rec'd PCT/PTO 21 OCT 2004

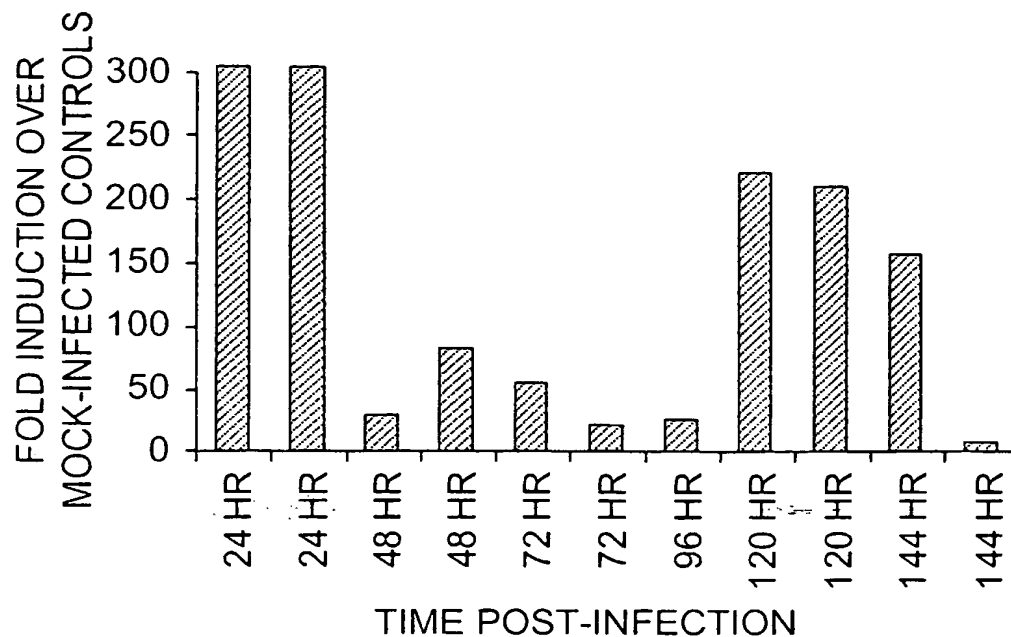


FIG. 32

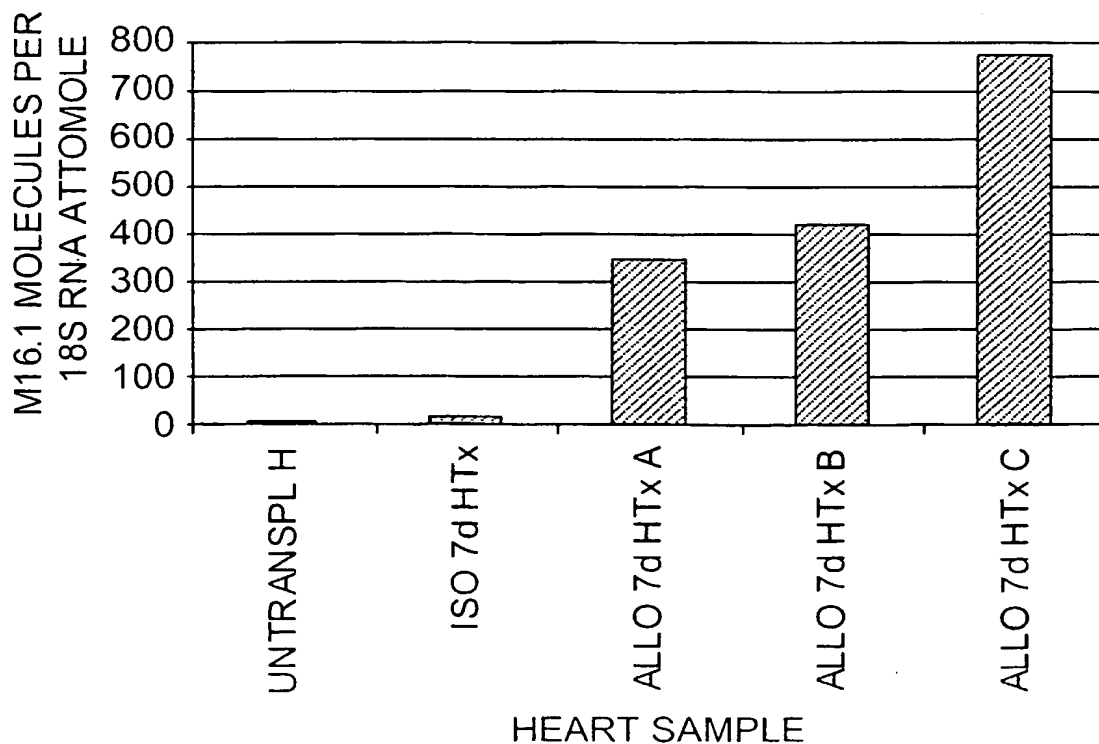


FIG. 33A
51/68

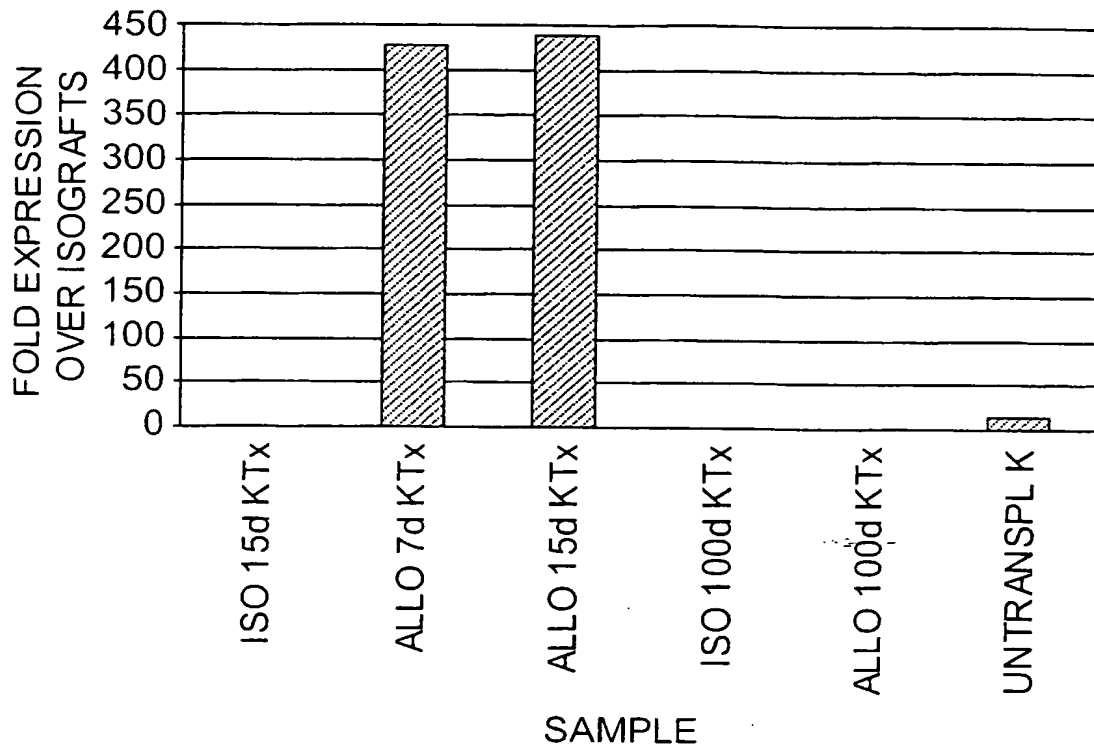


FIG. 33B

```

1  ATGAGGAAGCAAGAGGTGCGGACGGGCAGGGAGGCCGGCCAGGGCCACGG
51  TACGGGGCTCCCCAGCCGAGCAGGTGAAAGCCCTCATGGATCTGCTGGCTG
101 GGAAGGGCAGTCAAGGCTCCCAGGCCCCGCGAGGCCCTGGATAGGACACCG
151 GATGCCCCGCTGGGGCCCTGCAGCAATGACTCAAGGATACAGAGGCACCG
201 CAAGGCCCTGCTGAGCAAGGTGGGAGGTGGCCCCGAGCTGGGCGGACCCCT
251 GGCACAGGCTGGCCTCCCTCCTGCTGGTGGAGGGCCTGACGGACCTGCAG
301 CTGAGGGGAACACGACTTCACACAGGTGGAGGCCACCCGCGGGGGCGGGCA
351 CCCC GCCAGGACCGTCGCCCTGGACCGGCTCTTCCTGCCTCTCTCCCGGG
401 TGTCTGTCCCACCCCGGGTCTCCATCACTATCGGGGTGGCCGGCATGGGC
451 AAGACCACCCTGGTGAGGCACTTCGTCCGCCTCTGGGCCCATGGGCAGGT
501 CGGCAAGGACTTCTCGCTGGTGTGCTGCCTCTGACCTTCCGGGATCTCAACA
551 CCCACGAGAAGCTGTGTGCCGACCGACTCATCTGCTCGGTCTTCCCGCAC
601 GTCGGGGAGCCCAGCCTGGCGGTGGCAGTCCCAGCCAGGGCCCTCCTGAT
651 CCTGGACGGCTTGGATGAGTGCAGGACGCCTCTGGACTTCTCCAACACCG
701 TGGCCTGCACGGACCCAAAGAAGGAGATCCCGGTGGACCACCTGATCACC
751 AACATCATCCGTGGCAACCTCTTTCCGGAAGTTTCCATCTGGATCACCTC
801 CCGTCCCAGTGCATCTGGCCAGATCCCAGGGGGCCTGGTGGACCGGATGA
851 CGGAGATCCGGGGCTTTAACGAGGAGGAGATCAAGGTGTGTTTGGAGCAG
901 ATGTTCCCCGAGGACCAGGCCCTTCTGGGCTGGATGCTGAGCCAAGTGCA
951 GGCTGACAGGGCCCTGTACCTGATGTGCACCGTCCCAGCCTTCTGCAGGC
1001 TCACGGGGATGGCGCTAGGCCACCTGTGGCGCAGCAGGACGGGGCCCCAG
1051 GATGCAGAGCTGTGGCCCCCGAGGACCCTGTGCGAGCTCTACTCATGGTA
1101 CTTTAGGATGGCCCTCAGCGGGGAGGGGCAGGAGAAGGGCAAGGCAAGCC

```

FIG. 34A
52/68

1151 CTCGCATCGAGCAGGTGGCCCATGGTGGCCGCAAGATGGTGGGGACATTG
1201 GGCCGTCTGGCCTTCCATGGGCTGCTCAAGAAGAAATACGTGTTTTACGA
1251 GCAAGACATGAAGGCGTTTGGTGTAGACCTCGCTCTGCTGCAGGGCGCCC
1301 CGTGCAGCTGCTTCCCTGCAGAGAGAGGAGACGTTGGCATCGTCAGTGGCC
1351 TACTGCTTCACCCACCTGTCCCTGCAGGAGTTTGTGGCAGCCGCGTATTA
1401 CTATGGCGCATCCAGGAGGGCCATCTTCGACCTCTTCACTGAGAGCGGCG
1451 TATCCTGGCCCAGGCTGGGCTTCCCTCACGCATTTCAAGGAGCGCAGCCCAG
1501 CGGGCCATGCAGGCAGAGGACGGGAGGCTGGACGTGTTCCTGCGCTTCCT
1551 CTCCGGCCTCTTGTCTCCGAGGGTCAATGCCCTCCTGGCCGGCTCCCTGC
1601 TGGCCCAAGGCGAGCACCAGGCCTACCGGACCCAGGTGGCTGAGCTCCTG
1651 CAGGGCTGCCTGCGCCCCGATGCCGCGAGTCTGTGCACGGGCCATCAACGT
1701 GTTGCACTGCCTGCATGAGCTGCAGCACACCGAGCTGGCCCGCAGCGTGG
1751 AGGAGGCCATGGAGAGCGGGGCCCTGGCCAGGCTGACTGGTCCCGCGCAC
1801 CGCGCTGCCCTGGCCTACCTCCTGCAGGTGTCCGACGCCTGTGCCCAGGA
1851 GGCCAACCTGTCCCTGAGCCTCAGCCAGGGCGTCCTTCAGAGCCTGCTGC
1901 CCCAGCTGCTCTACTGCCGGAAGCTCAGGCTGCGTTACTTCAGTCTCTCC
1951 CGTCGCCTGGTCATCTTCTCCCTGTGTCTGTCTCCACATGGTGTCTGTCT
2001 CTCTTTTTTTTTGAGATGGAGTCTTGCTCTGTGCGCCAGGCTGGAATACA
2051 GTGGCGCGATCTCAGCTCACTGCAAACGCTGCCTCCTGGGTTCAAGCGAT
2101 TCTCCTGCCTCAGCCTCCCTAGTAGCTGGGATTACAGGTGCCCGCCATCA
2151 TGCCTGGCTAATTTTTGTGTTTTAGTAGAGACGGGGTTTCACCATGTTG
2201 GCCAGGCTGCTCTCAAACCTCTGACCTCAG (SEQ ID NO:25)

FIG. 34B

1 MRKQEVRTGREAGQGHGTGSPAQVVKALMDLLAGKGSQGSQAPQALDRTP
51 DAPLGPCSNDRIQRHRKALLSKVGGGPELGGPWHRLASLLLVEGLTDLQ
101 LREHDFTQVEATRGGGHPARTVALDRLFLPLSRVSVPPRVSITIGVAGMG
151 KTTLVRRHFVRLWAHGQVGKDFSLVLPLTFRDLNTHEKLCADRILCSVFP
201 VGEPSLAVAVPARALLILDGLDECRTPLDFSNTVACTDPKKEIPVDHLIT
251 NIIRGNLFPEVSIWITSRPSASQIPGGLVDRMTEIRGFNEEEIKVCLEQ
301 MFPEDQALLGWMLSQVQADRALYLMCTVPAFCRLTGMA LGHLWRSRTGPQ
351 DAELWPPRTLCELYSWYFRMALSGEGQEKGKASPRIEQVAHGGRKMVGTL
401 GRLAFHGLLKKKYVFYEQDMKAFGVDLALLQGAPCSCFLQREETLASSVA
451 YCFTHLSLQEFVAAAYYYGASRAIFDLFTESGVSWPRLGFLTHFRSAAQ
501 RAMQAEDGRLDVFLRFLSGLLSPRVNALLAGSLLAQGEHQAYRTQVAELL
551 QGCLRPDAAVCARAINVLHCLHELOHTELARSVEEAMESGALARLTGPAH
601 RAALAYLLQVSDACAQEANLSLSLSQGV LQSLLPQLLYCRKLRLRYFSL
651 RRLVIFSLCLSPHGAVLSFFLRWSLALSPRLEYSGAISAHCKRCLLGSSD
701 SPASASLVAGITGARHHAWLIFVFLVETGFHHVGAALKLLTS
(SEQ ID NO:26)

FIG. 34C

Rec'd PCT/PTO 21 OCT 2004

1 ATTCCCAGGGCATCTACCACCACGCAGCTGGAGCAGGGCTGAGCCCAGGA
51 GCATGGAGATGGACGCCCCCAGGCCCCCAGTCTTGCTGTCCCTGGAGCA
101 GCATCGAGGCCCCGGGAGAACTGTGGACAACGGAAGGCTGAGCCCCATCCA
151 TTGAGTTCTTGGGGCCCCACTGGAGGGGCTGCTGTGGCCAGGGTGCACGG
201 TCACAAATGAAGACACCAAGGCGCAGAGAGGTGACTCAGCCTGCCCTCAG
251 TCACCTATCTGCTCCTGGAGGTGATCCCCGACTCCATGAGGAAGCAAGAG
301 GTGCGGACGGGCAGGGAGGCCGGCCAGGGCCACGGTACGGGCTCCCCAGC
351 CGAGCAGGTGAAAGCCCTCATGGATCTGCTGGCTGGGAAGGGCAGTCAAG
401 GCTCCCAGGCCCCCGCAGGCCCTGGATAGGACACCGGATGCCCCGCTGGGG
451 CCCTGCAGCAATGACTCAAGGATACAGAGGCACCGCAAGGCCCTGCTGAG
501 CAAGGTGGGAGGTGGCCCCGAGCTGGGCGGACCCTGGCACAGGCTGGCCT
551 CCCTCCTGCTGGTGGAGGGCCTGACGGACCTGCAGCTGAGGGAACACGAC
601 TTCACACAGGTGGAGGCCACCCGCGGGGGCGGGCACCCCGCCAGGACCGT
651 CGCCCTGGACCGGCTCTTCCTGCCTCTCTCCCGGGTGTCTGTCCCACCCC
701 GGGTCTCCATCACTATCGGGGTGGCCGGCATGGGCAAGACCACCTGGTG
751 AGGCACTTCGTCCGCCTCTGGGCCCATGGGCAGGTGGCAAGGACTTCTC
801 GCTGGTGTCTGCCTCTGACCTTCCGGGATCTCAACACCCACGAGAAGCTGT
851 GTGCCGACCGACTCATCTGCTCGGTCTTCCCGCACGTGGGGAGCCCAGC
901 CTGGCGGTGGCAGTCCCAGCCAGGGCCCTCCTGATCCTGGACGGCTTGGA
951 TGAGTGCAGGACGCCTCTGGACTTCTCCAACACCGTGGCCTGCACGGACC
1001 CAAAGAAGGAGATCCCGGTGGACCACCTGATCACCAACATCATCCGTGGC
1051 AACCTCTTTCCGGAAGTTTCCATCTGGATCACCTCCCGTCCCAGTGCATC
1101 TGGCCAGATCCCAGGGGGCCTGGTGGACCGGATGACGGAGATCCGGGGCT
1151 TTAACGAGGAGGAGATCAAGGTGTGTTTGGAGCAGATGTTCCCCGAGGAC
1201 CAGGCCCTTCTGGGCTGGATGCTGAGCCAAGTGCAGGCTGACAGGGCCCT
1251 GTACCTGATGTGCACCGTCCCAGCCTTCTGCAGGCTCACGGGGATGGCGC
1301 TAGGCCACCTGTGGCGCAGCAGGACGGGGCCCCAGGATGCAGAGCTGTGG
1351 CCCCCGAGGACCCTGTGCGAGCTCTACTCATGGTACTTTAGGATGGCCCT
1401 CAGCGGGGAGGGGAGGAGAGAAGGGCAAGGCCCTCGCATCGAGCAGG
1451 TGGCCCATGGTGGCCGCGAAGATGTTGGGGACATTTGGGGCCGTCTGGCCCTC
1501 CATGGGCTGCTCAAGAAGAAATACGTGTTTTACGAGCAAGACATGAAGGC
1551 GTTTGGTGTAGACCTCGCTCTGCTGCAGGGCGCCCCGTGCAGCTGCTTCC
1601 TGCAGAGAGAGGAGACGTTGGCATCGTCAGTGGCCTACTGCTTCACCCAC
1651 CTGTCCCTGCAGGAGTTTGTGGCAGCCGCGTATTACTATGGCGCATCCAG
1701 GAGGGCCATCTTCGACCTCTTCACTGAGAGCGGCGTATCCTGGCCCAGGC
1751 TGGGCTTCCTCACGCATTTAGGAGCGCAGCCAGCGGGCCATGCAGGCA
1801 GAGGACGGGAGGCTGGACGTGTTCTGCGCTTCTCTCCGGCCTCTTGTC
1851 TCCGAGGGTCAATGCCCTCCTGGCCGGCTCCCTGCTGGCCCAAGGCGAGC
1901 ACCAGGCCTACCGGACCCAGGTGGCTGAGCTCCTGCAGGGCTGCCTGCGC
1951 CCCGATGCCGCAGTCTGTGCACGGGCCATCAACGTGTTGCACTGCCTGCA
2001 TGAGCTGCAGCACACCGAGCTGGCCCCGACGCTGGAGGAGGCCATGGAGA
2051 GCGGGGGCCCTGGCCAGGCTGACCGGTCCCGCGCACCGCGCTGCCCTGGCC
2101 TACCTCCTGCAGGTGTCCGACGCTGTGCCCAGGAGGCCAACCTGTCCCT
2151 GAGCCTCAGCCAGGGCGTCTTTCAGAGCCTGCTGCCCCAGCTGCTCTACT
2201 GCCGGAAGCTCAGGCTGGACACCAACCAGTTCCAGGACCCCGTGATGGAG
2251 CTGCTGGGCAGCGTGCTGAGTGGGAAGGACTGTCGCATTTCAGAAGATCAG
2301 CTTGGCGGAGAACCAGATCAGTAACAAAGGGGGCCAAAGCTCTGGCCAGAT
2351 CCCTCTTGGTCAACAGAAGTCTGACCTCTCTGGACCTCCGCGGTAACCTC
2401 ATTGGACCACAAGGGGGCCAAAGGCGCTGGCAGACGCTTTGAAGATCAACCG
2451 CACCCTGACCTCCCTGAGCCTCCAGGGCAACACCGTTAGGGATGATGGTG
2501 CCAGGTCCATGGCTGAGGCCTTGGCCTCCAACCGGACCCCTCTCCATGCTG

2801 CACCTGCAGAAGAACAGCATCGGGCCCATGGGAGCCCAGCGGATGGCAGA
 2851 TGCCTTGAAGCAGAACAGGAGTCTGAAAGAGCTCATGTTCTCCAGTAATA
 2901 GTATTGGTGATGGAGGTGCCAAGGCCCTGGCTGAGGCCCTGAAGGTGAAC
 2951 CAGGGCCTGGAGAGCCTGGACCTGCAGAGCAATTCCATCAGTGACGCAGG
 3001 AGTGGCAGCACTGATGGGGGCCCTCTGCACCAACCAGACCCTCCTCAGCC
 3051 TCAGCCTTCGAGAAAACCTCCATCAGTCCCGAGGGAGCCCAGGCCATCGCT
 3151 CATGCCCTCTGCGCCAACAGCACCCCTGAAGAACCTGGACCTGACAGCCAA
 3201 CCTCCTCCACGACCAGGGTGCCCGGGCCATCGCAGTGGCAGTGAGAGAAA
 3251 ACCGCACCCTCACCTCCCTTCACCTGCAGTGGAACCTCATCCAGGCCGGC
 3301 GCTGCCCAGGCCCTGGGACAAGCACTACAGCTCAACAGGAGCCTCACCAG
 3351 CTTAGATTTACAGGAGAACGCCATCGGGGATGACGGAGCGTGTGCGGTGG
 3401 CCCGTGCACTGAAGGTCAACACAGCCCTCACTGCTCTCTATCTCCAGGTG
 3451 GCCTCAATTGGTGCTTCAGGCGCCCAGGTGCTAGGGGAAGCCTTGGCTGT
 3501 GAACAGAACCTTGGAGATTCTCGACTTAAGAGGAAATGCCATTGGGGTGG
 3551 CTGGAGCCAAAGCCCTGGCAAATGCTCTGAAGGTAAACTCAAGTCTCCGG
 3601 AGACTCAATCTTCAAGAGAATTCTCTGGGGATGGACGGGGCGATATGCAT
 3651 TGCCACAGCACTGTCTGGAAACCACAGGCTCCAGCATATCAATCTCCAGG
 3701 GAAACCACATTGGGGACTCCGGGGCCAGGATGATCTCAGAGGCCATCAAG
 3751 ACAAATGCTCCACGTGCACTGTTGAAATGTGATCCTGG
 (SEQ ID NO: 27)

FIG. 34E

1 MRKQEVRTGREAGQGHGTGSPAQVVKALMDLLAGKGSQGSQAPQALDRTP
 51 DAPLGPCSNDSRIQRHRKALLSKVGGGPPELGGPWHRLASLLLVEGLTDLQ
 101 LREHDFEQVEATRGGGHPARTVALDRLFLPLSRVSVPPRVSIITIGVAGMG
 151 KTTLVHRHFVRLWAHGQVGKDFSLVPLTFRDLNTHEKLCADRILICSVFPH
 201 VGEPSLAVAVPARALLILDGLDECRTPLDFSNTVACTDPKKEIPVDHLIT
 251 NIIRGNLFPEVSIWITSRPSASGQIPGGLVDRMTEIRGFNEEEIKVCLEQ
 301 MFPEDQALLGWMLSQVQADRALYLMCTVPAFCRLTGMALGHLWRSRTGPQ
 351 DAELWPPRTLCELYSWYFRMALSGEGQEKGPRIEQVAHGGRKMVGTL
 401 GRLAFHGLLKKKYVFYEQDMKAFGVLDLALLQGAPCSCFLQREETLASSVA
 451 YCFTHLSLQEFVAAAYYYGASRAIFDLFTESGVSWPRLGFLTHFRSAAQ
 501 RAMQAEDGRLDVFLRFLSGLLSPRVNALLAGSLLAQGEHQAYRTQVAELL
 551 QGCLRPDAAVCARAINVLHCLHELQHTELARSVEEAMESGALARLTGPAH
 601 RAALAYLLQVSDACAQEANLSLSLSQGVLSLLPQLLYCRKLRLDTNQFQ
 651 DPVMELLGSVLSGKDCRIQKISLAENQISNKGAKALARSLLVNRSLTSLD
 701 LRGNISIGPQAKALADALKINRTLTSLSLQGNVTRDDGARSMAEALASNR
 751 TLSMLHLQKNSIGPMGAQRMADALKQNRSLKELMFSSNSIGDGGAKALAE
 801 ALKVNQGLSDDLQSNISDAGVAALMGALCTNQTLTSLSLRENSISPEG
 851 AQAIAHALCANSTLKNLDTANLLHDQGARAIAVAVRENRTLTSLHLQWN
 901 FIQAGAAQALGQALQLNRSLTSLDLQENAIGDDGACAVARALKVNTALTA
 951 LYLQVASIGASGAQVLGEALAVNRTLEILDLRGNAIGVAGAKALANALKV
 1001 NSSLRLNLQENSLGMDGAICIATALSNGHRLQHINLQGNHIGDSGARM
 1051 SEAIKTNAPTCTVEM (SEQ ID NO: 28)

FIG. 34F

Rec'd PCT/PTO 21 OCT 2004

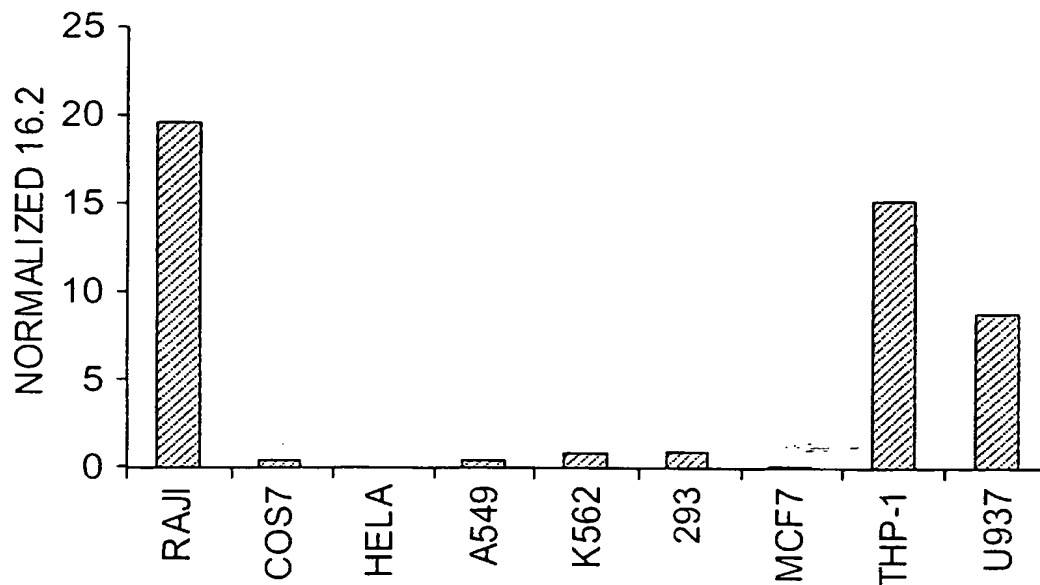


FIG. 35A

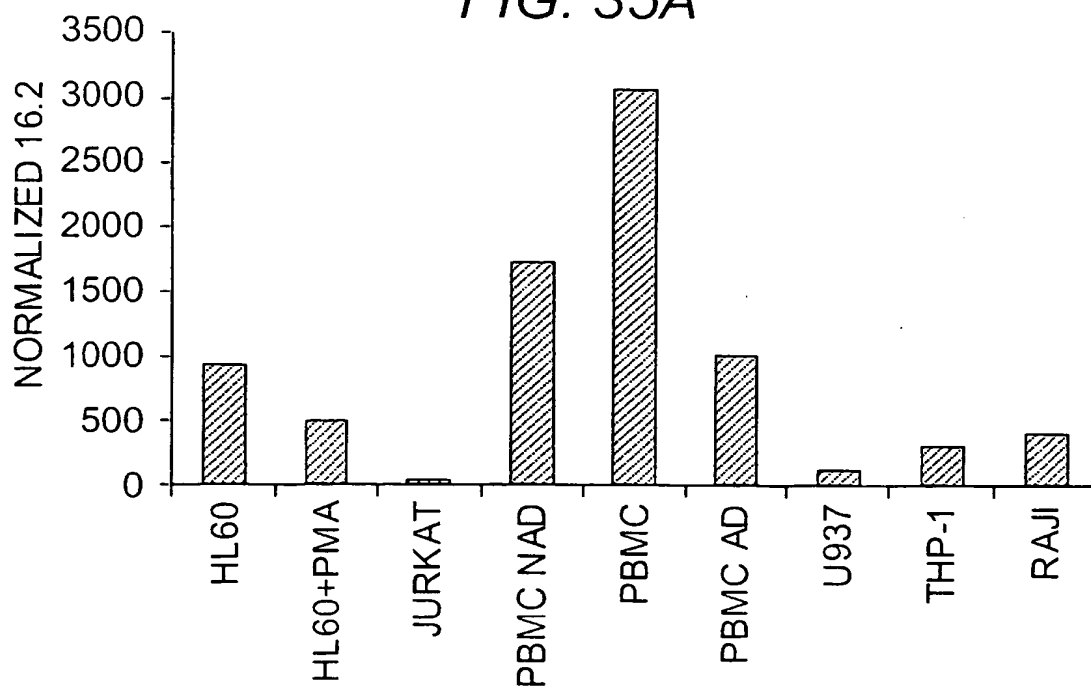


FIG. 35B

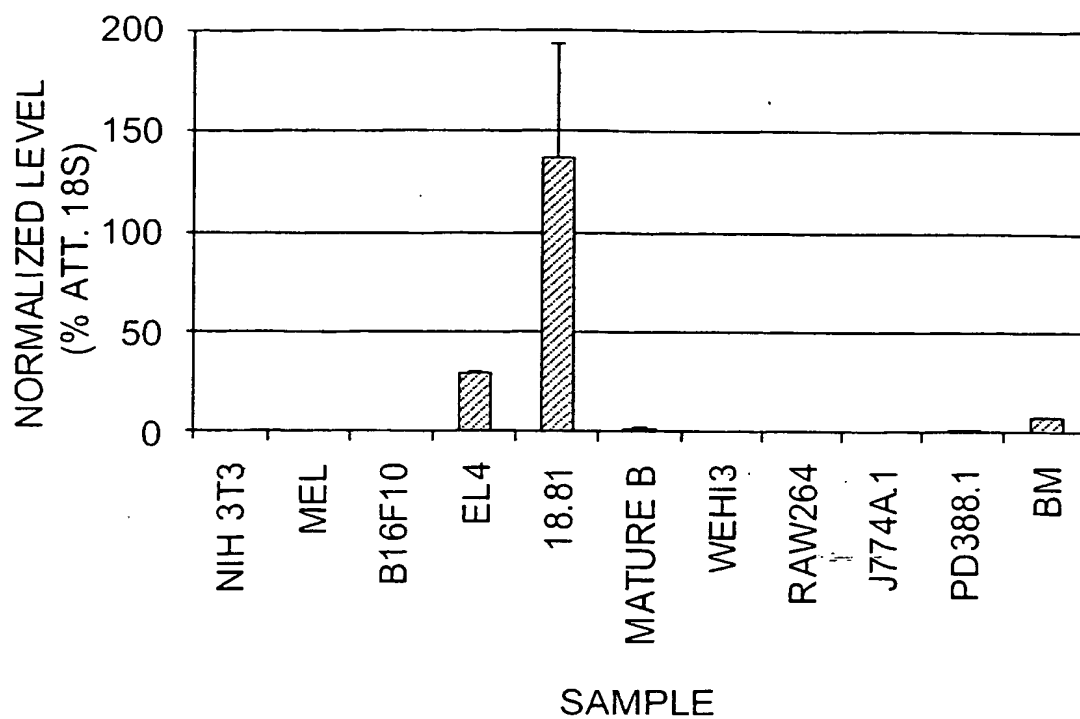


FIG. 36A

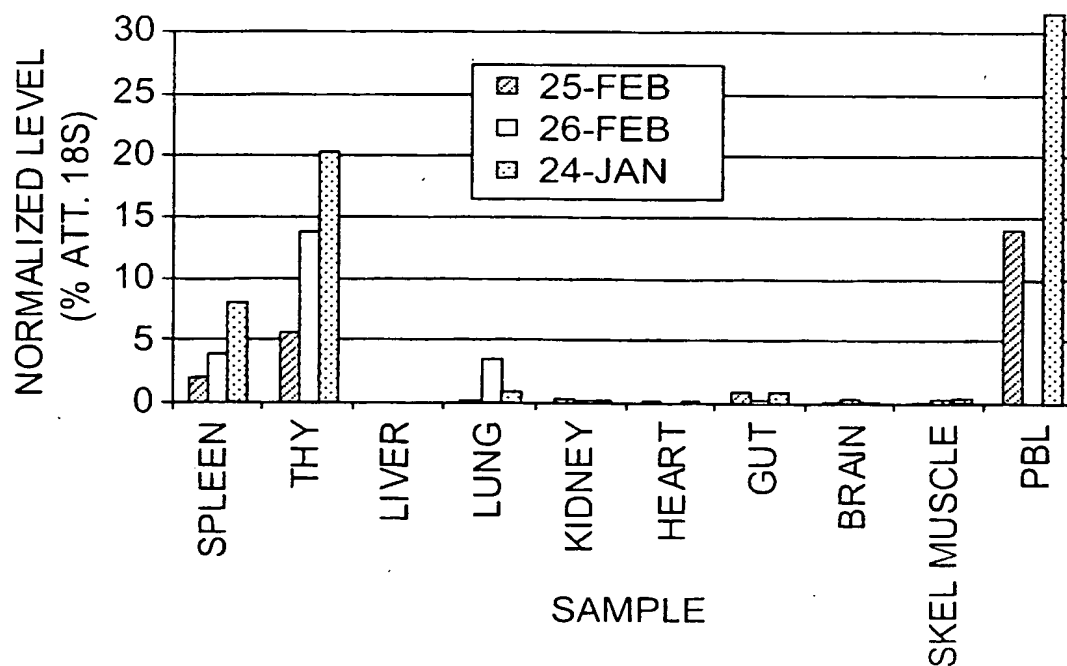


FIG. 36B

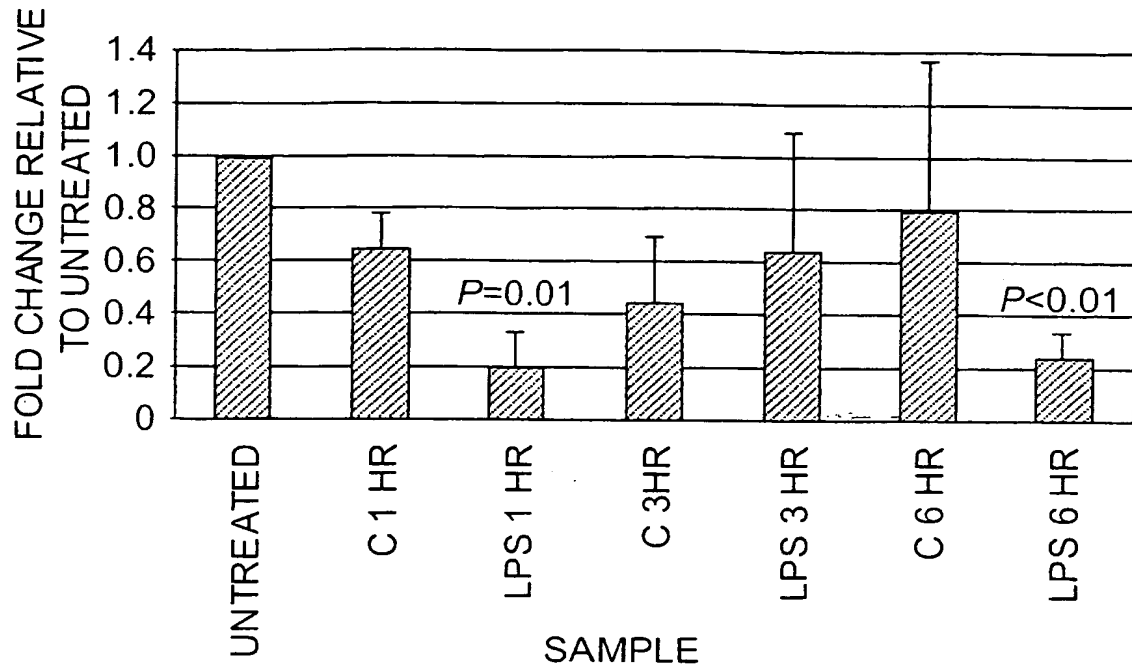


FIG. 36C

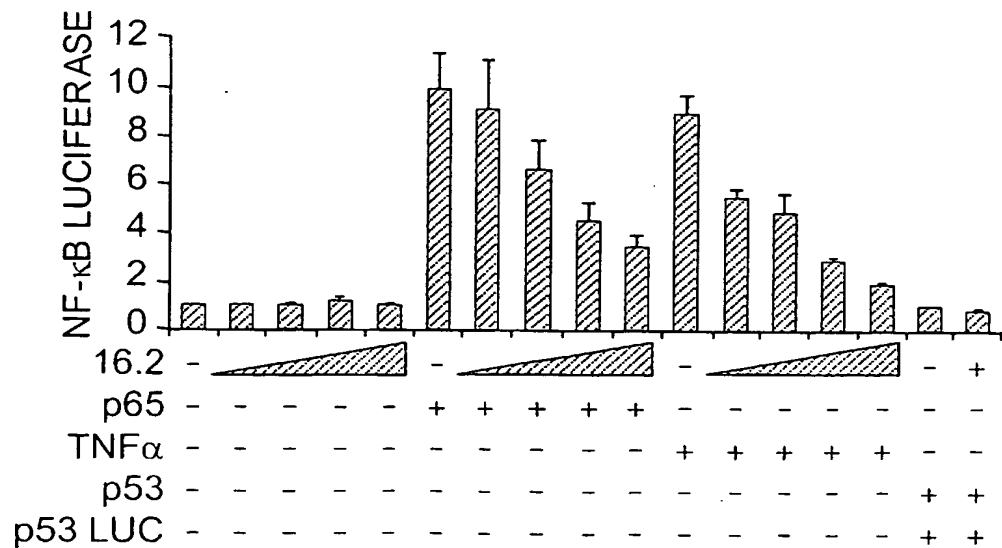


FIG. 37A

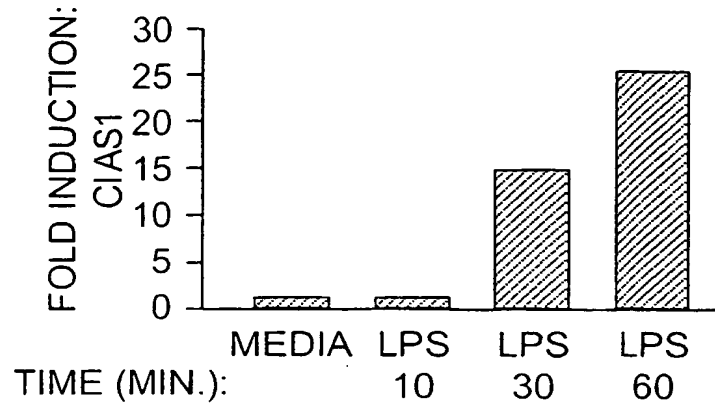


FIG. 38B

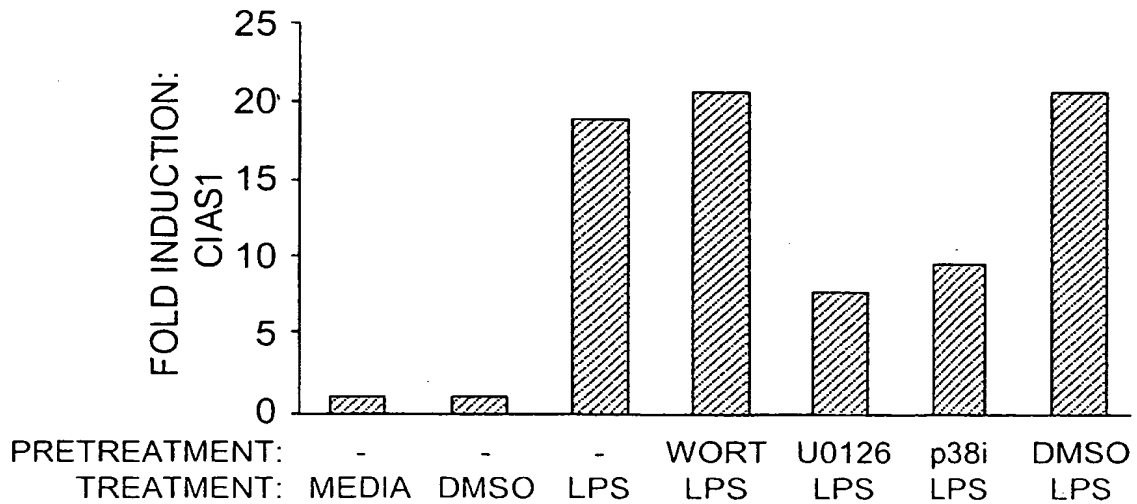


FIG. 38C

FIG. 39A

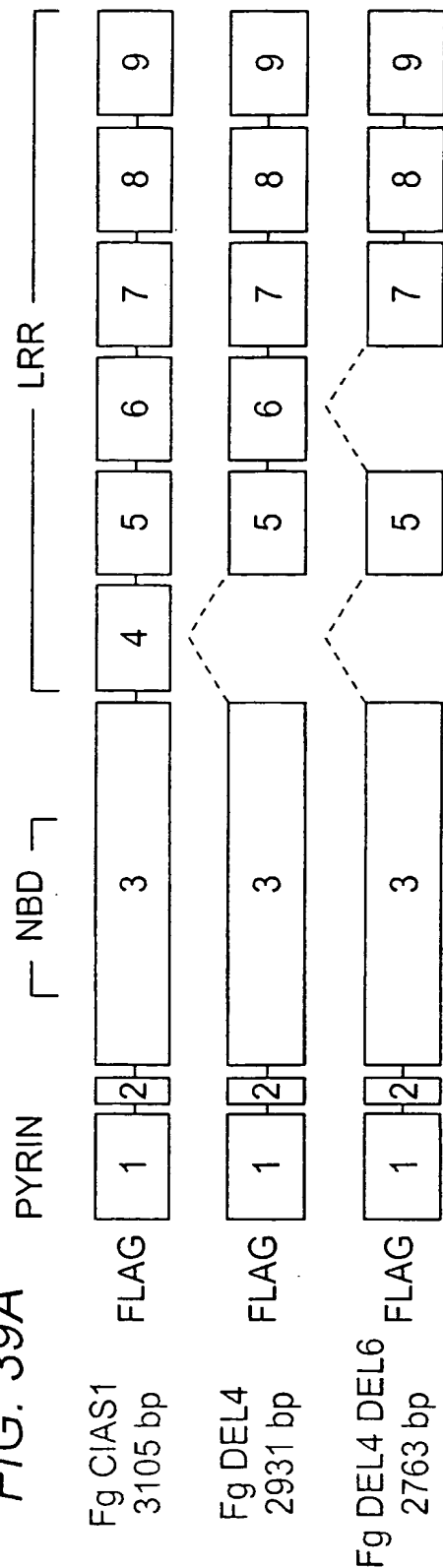
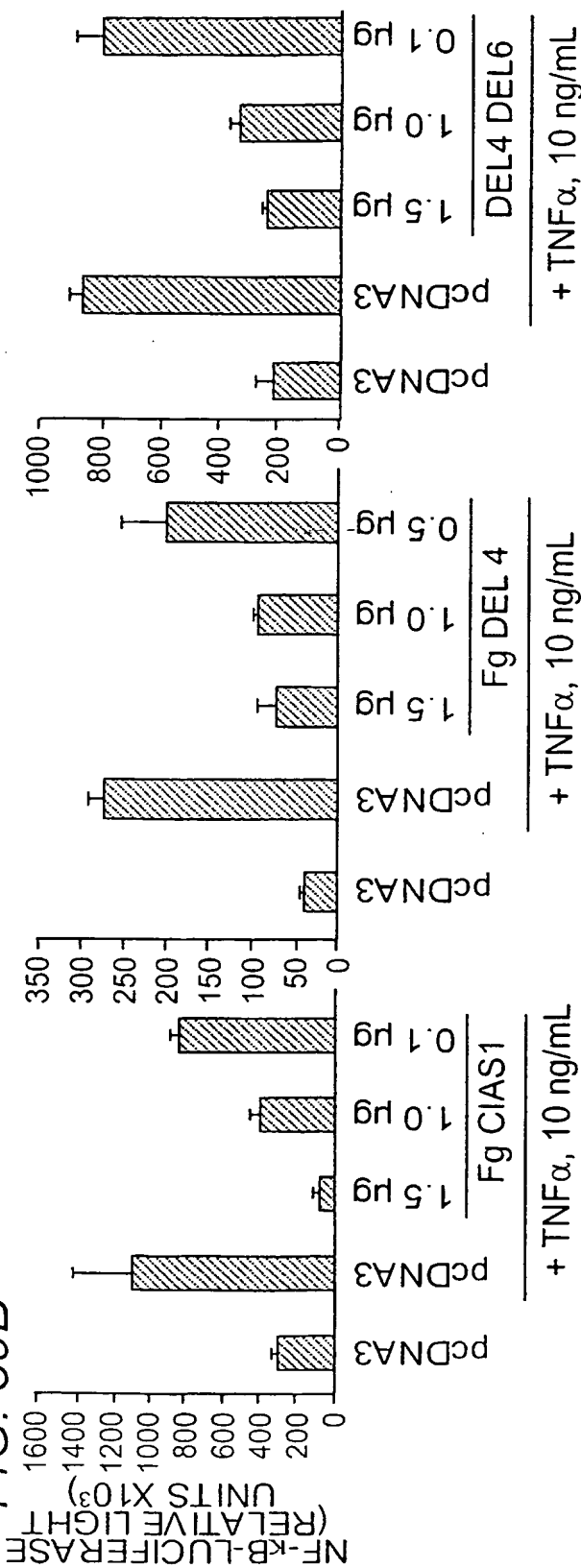


FIG. 39B



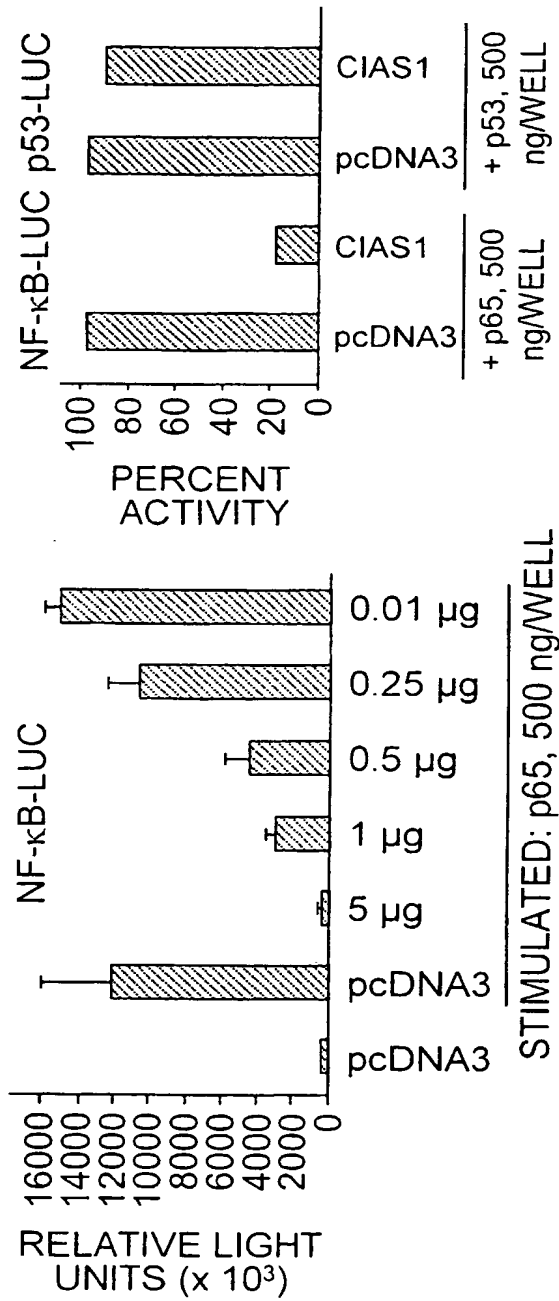


FIG. 39C

FIG. 40

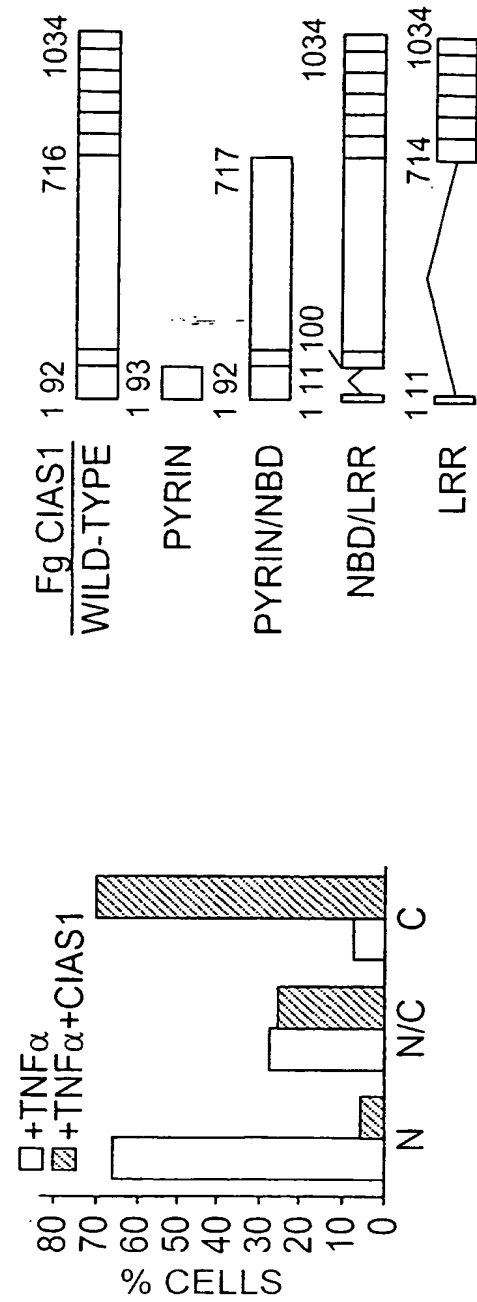
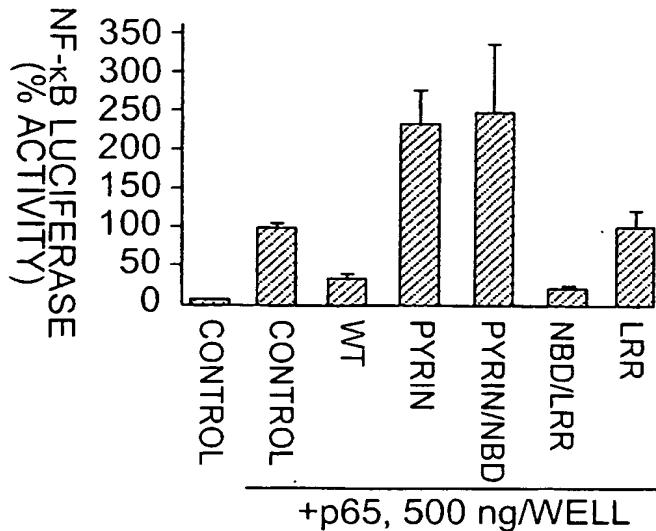


FIG. 41A

FIG. 41B



1 ATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCTGGAGGACCTGGAGGA
 51 TGTGGACTTGAAGAAATTTAAGATGCACTTAGAGGACTATCCTCCCCAGA
 101 AGGGCTGCATCCCCCTCCCGAGGGGTCAGACAGAGAAGGCAGACCATGTG
 151 GATCTAGCCACGCTAATGATCGACTTCAATGGGGAGGAGAAGGCGTGGGC
 201 CATGGCCGTGTGGATCTTCGCTGCGATCAACAGGAGAGACCTTTATGAGA
 251 AAGCAAAAAGAGATGAGCCGAAGTGGGGTTAG (SEQ ID NO:29)

FIG. 42A

1 MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLRGQTEKADHV
 51 DLATLMIDFNREEKAWAMAVWIFAAINRRDLYEKAKRDEPKWG
 (SEQ ID NO:30)

FIG. 42B

1 ATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCTGGAGGACCTGGAGGA
 51 TGTGGACTTGAAGAAATTTAAGATGCACTTAGAGGACTATCCTCCCCAGA
 101 AGGGCTGCATCCCCCTCCCGAGGGGTCAGACAGAGAAGGCAGACCATGTG
 151 GATCTAGCCACGCTAATGATCGACTTCAATGGGGAGGAGAAGGCGTGGGC
 201 CATGGCCGTGTGGATCTTCGCTGCGATCAACAGGAGAGACCTTTATGAGA
 251 AAGCAAAAAGAGATGAGCCGAAGTGGGGTTTCAGATAATGCACGTGTTTCG
 301 AATCCCCTGTGATATGCCAGGAAGACAGCATTGAAGAGGAGTGGATGGG
 351 TTTACTGGAGTACCTTTTCGAGAATCTCTATTTGTAAAATGAAGAAAGATT
 401 ACCGTAAGAAGTACAGAAAGTACGTGAGAAGCAGATTCCAGTGCATTGAA
 451 GACAGGAATGCCCCGTCTGGGTGAGAGTGTGAGCCTCAACAAACGCTACAC
 501 ACGACTGCGTCTCATCAAGGAGCACCGGAGCCAGCAGGAGAGGGAGCAGG
 551 AGCTTCTGGCCATCGGCAAGACCAAGACGTGTGAGAGCCCCGTGAGTCCC
 601 ATTAAGATGGAGTTGCTGTTTGACCCCGATGATGAGCATTCTGAGCCTGT
 651 GCACACCGTGGTGTTCAGGGGGCGGCAGGGATTGGGAAAACAATCCTGG
 701 CCAGGAAGATGATGTTGGACTGGGCGTCGGGGACACTCTACCAAGACAGG
 751 TTTGACTATCTGTTCTATATCCACTGTCGGGAGGTGAGCCTTGTGACACA
 801 GAGGAGCCTGGGGGACCTGATCATGAGCTGCTGCCCCGACCCCAACCCAC
 851 CCATCCACAAGATCGTGAGAAAACCCTCCAGAATCCTCTTCCTCATGGAC
 901 GGCTTCGATGAGCTGCAAGGTGCCTTTGACGAGCACATAGGACCGCTCTG
 951 CACTGACTGGCAGAAGGCCGAGCGGGGAGACATTCTCCTGAGCAGCCTCA
 1001 TCAGAAAGAAGCTGCTTCCCGAGGCCTCTCTGCTCATCACCACGAGACCT

FIG. 42C

1051 GTGGCCCTGGAGAACTGCAGCACTTGCTGGACCATCCTCGGCATGTGGA
 1101 GATCCTGGGTTTCTCCGAGGCCAAAAGGAAAGAGTACTTCTTCAAGTACT
 1151 TCTCTGATGAGGCCCAAGCCAGGGCAGCCTTCAGTCTGATTTCAGGAGAAC
 1201 GAGGTCTCTTCACCATGTGCTTCATCCCCCTGGTCTGCTGGATCGTGTG
 1251 CACTGGACTGAAACAGCAGATGGAGAGTGGCAAGAGCCTTGCCCAGACAT
 1301 CCAAGACCACCACCGCGGTGTACGTCTTCTTCTTCCAGTTTGCTGCAG
 1351 CCCCAGGGAGGGAGCCAGGAGCACGGCCTCTGCGCCACCTCTGGGGGCT
 1401 CTGCTCTTTGGCTGCAGATGGAATCTGGAACCAGAAAATCCTGTTTGAGG
 1451 AGTCCGACCTCAGGAATCATGACTGCAGAAGGCGGATGTGTCTGCTTTC
 1501 CTGAGGATGAACCTGTTCCAAAAGGAAGTGGACTGCGAGAAGTTCTACAG
 1551 CTTTCATCCACATGACTTTCCAGGAGTTCTTTGCCGCCATGTACTACCTGC
 1601 TGGAAGAGGAAAAGGAAGGAAGGACGAACGTTCCAGGGAGTCGTTTGAAG
 1651 CTTCCCAGCCGAGACGTGACAGTCCTTCTGGAAACTATGGCAAATTCGA
 1701 AAAGGGGTATTTGATTTTGTGTACGTTTCTTCTTTGGCCTGGTAAACC
 1751 AGGAGAGGACCTCCTACTTGAGAGAAGAAATTAAGTTGCAAGATCTCTCAG
 1801 CAAATCAGGCTGGAGCTGCTGAAATGGATTGAAGTGAAAGCCAAAGCTAA
 1851 AAAGCTGCAGATCCAGCCCAGCCAGCTGGAATTGTTCTACTGTTTGTACG
 1901 AGATGCAGGAGGAGGACTTCGTGCAAAGGGCCATGGAATATTTCCCAAG
 1951 ATTGAGATCAATCTCTCCACCAGAATGGACCACATGGTTTCTTCTTTTG
 2001 CATTGAGAACTGTCATCGGGTGGAGTCACTGTCCCTGGGGTTTCTCCATA
 2051 ACATGCCCAAGGAGGAAGAGGAGGAGGAAAAGGAAGGCCGACACCTTGAT
 2101 ATGGTGCAGTGTGTCTCCCAAGCTCCTCTCATGCTGCCTGTTCTCATGG
 2151 ATAG (SEQ ID NO:31)

FIG. 42D

1 MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIPLPQGTEKADHV
 51 DLATLMIDFNGEKAWAMAVWIFAAINRRDLYEKA KRDEPKWGS DNARVS
 101 NPTVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRKYVRSRFQCI E
 151 DRNARLGESVSLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSP
 201 IKMELLFDPDDEHSEPVHTVVFQGAAGIGKTI LARKMMLDWASGTL YQDR
 251 FDYLFYIHCREVSLVTQ RSLGDLIMSCCPDPNPPIHKIVRKPSRI LFLMD
 301 GFDELQGA FDEHIGPLCTDWQKAERGDI LLSSLIRKKLLPEASLLITTRP
 351 VALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEA QARA AFSLIQEN
 401 EVLFTMCFIPLVCWIVCTGLKQOMESGKSLAQTSKTTTAVYVFFLSSLLQ
 451 PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAF
 501 LRMNLFQKEVDCEKFYSFIHMTFQEFFAAMYLL EEEKEGR TNVPGSRLK
 551 LPSRDVTVLLENYGKFEKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQ
 601 QIRLELLKWIEVKAKAKKLQIQPSQLELFYCLYEMQEEDFVQRAMDYFPK
 651 IEINLSTRMDH MVSSFCIENCHRVESLSLGLHNMPKEEEEEKEGRHLD
 701 MVQCVLPSSSHAACSHG (SEQ ID NO:32)

FIG. 42E

1 ATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCCCACTGTGATATGCCA
 51 GGAAGACAGCATTGAAGAGGAGTGGATGGGTTTACTGGAGTACCTTTTCCA
 101 GAATCTCTATTTGTAAAATGAAGAAAGATTACCGTAAGAAGTACAGAAAG
 151 TACGTGAGAAGCAGATTCCAGTGCATTGAAGACAGGAATGCCCGTCTGGG
 201 TGAGAGTGTGAGCCTCAACAAACGCTACACACGACTGCGTCTCATCAAGG
 251 AGCACCCGAGCCAGCAGGAGAGGGAGCAGGAGCTTCTGGCCATCGGCAAG
 301 ACCAAGACGTGTGAGAGCCCCGTGAGTCCCATTAAGATGGAGTTGCTGTT
 351 TGACCCCGATGATGAGCATTCTGAGCCTGTGCACACCGTGGTGTTCAGG
 401 GGGCGGCAGGGATTGGGAAAACAATCCTGGCCAGGAAGATGATGTTGGAC

FIG. 42F

451 TGGGCGTCGGGGACACTCTACCAAGACAGGTTTGACTATCTGTTCTATAT
501 CCACTGTCGGGAGGTGAGCCTTGTGACACAGAGGAGCCTGGGGGACCTGA
551 TCATGAGCTGCTGCCCCGACCCAAACCCACCCATCCACAAGATCGTGAGA
601 AAACCCCTCCAGAATCCTCTTCCTCATGGACGGCTTCGATGAGCTGCAAGG
651 TGCCTTTGACGAGCACATAGGACCGCTCTGCACTGACTGGCAGAAGGCCG
701 AGCGGGGAGACATTCTCCTGAGCAGCCTCATCAGAAAGAAGCTGCTTCCC
751 GAGGCCTCTCTGCTCATCACACGAGACCTGTGGCCCTGGAGAAACTGCA
801 GCACTTGCTGGACCATCCTCGGCATGTGGAGATCCTGGGTTTCTCCGAGG
851 CCAAAGGAAAGAGTACTTCTTCAAGTACTTCTCTGATGAGGCCCAAGCC
901 AGGGCAGCCTTCAGTCTGATTACAGGAGAACGAGGTCTCTTACCATTGTG
951 CTTTCATCCCCCTGGTCTGCTGGATCGTGTGCACTGGACTGAAACAGCAGA
1001 TGGAGAGTGGCAAGAGCCTTGCCAGACATCCAAGACCACCACCGCGGTG
1051 TACGTCTTCTTCCTTTCCAGTTTGGCTGCAGCCCCGGGGAGGGAGCCAGGA
1101 GCACGGCCTCTGCGCCACCTCTGGGGGCTCTGCTCTTTGGCTGCAGATG
1151 GAATCTGGAACCAGAAAATCCTGTTTGAGGAGTCCGACCTCAGGAATCAT
1201 GGAATGCAAGGCGGATGTGTCTGCTTTCCTGAGGATGAACCTGTTCCA
1251 AAAGGAAGTGGACTGCGAGAAGTTCTACAGCTTCATCCACATGACTTTCC
1301 AGGAGTTCTTTGCCGCCATGTACTACCTGCTGGAAGAGGAAAAGGAAGGA
1351 AGGACGAACGTTCCAGGGAGTCGTTTGAAGCTTCCCAGCCGAGACGTGAC
1401 AGTCCTTCTGGAAAACATATGGCAAATTCGAAAAGGGGTATTTGATTTTGT
1451 TTGTACGTTTCTCTTTGGCCTGGTAAACCAGGAGAGGACCTCCTACTTG
1501 GAGAAGAAATTAAGTTGCAAGATCTCTCAGCAAATCAGGCTGGAGCTGCT
1551 GAAATGGATTGAAGTGAAAGCCAAAGCTAAAAAGCTGCAGATCCAGCCCA
1601 GCCAGCTGGAATTGTTCTACTGTTTGTACGAGATGCAGGAGGAGGACTTC
1651 GTGCAAAGGGCCATGGACTATTTCCCCAAGATTGAGATCAATCTCTCCAC
1701 CAGAATGGACCACATGGTTTCTTCCCTTTTGCATTGAGAACTGTCATCGGG
1751 TGGAGTCACTGTCCCTGGGGTTTCTCCATAACATGCCCAAGGAGGAAGAG
1801 GAGGAGGAAAAGGAAGGCCGACACCTTGATATGGTGCAGTGTGTCTCTCC
1851 AAGCTCCTCTCATGCTGCCTGTTCTCATGGATTGGTGAACAGCCACCTCA
1901 CTTCCAGTTTTTGGCGGGGCTCTTTTTCAGTTCTGAGCACCAGCCAGAGT
1951 CTAAGTGAATTGGACCTCAGTGACAATTCTCTGGGGGACCCAGGGATGAG
2001 AGTGTGTGTGAAACGCTCCAGCATCCTGGCTGTAACATTCGGAGATTGT
2051 GGTGGGGGCGCTGTGGCCTCTCGCATGAGTGCTGCTTCGACATCTCCTTG
2101 GTCCTCAGCAGCAACCAGAAGCTGGTGGAGCTGGACCTGAGTGACAACGC
2151 CCTCGGTGACTTCGGAATCAGACTTCTGTGTGTGGGACTGAAGCACCTGT
2201 TGTGCAATCTGAAGAAGCTCTGGTTGGTCAGCTGCTGCCTCACATCAGCA
2251 TGTGTCAGGATCTTGCATCAGTATTGAGCACCAGCCATTCCCTGACCAG
2301 ACTCTATGTGGGGGAGAATGCCTTGGGAGACTCAGGAGTCGCAATTTTAT
2351 GTGAAAAAGCCAAGAATCCACAGTGTAACCTGCAGAACTGGGGTTGGTG
2401 AATTCTGGCCTTACGTCAGTCTGTTGTTTCAGCTTTGTCTCGGTACTCAG
2451 CACTAATCAGAATCTCACGCACCTTTACCTGCGAGGCAACACTCTCGGAG
2501 ACAAGGGGATCAAACACTACTCTGTGAGGGACTCTTGACCCCCGACTGCAAG
2551 CTTACAGGTGTTGGAATTAGACAACTGCAACCTCACGTCACACTGCTGCTG
2601 GGATCTTTCCACACTTCTGACCTCCAGCCAGAGCCTGCGAAAGCTGAGCC
2651 TGGGCAACAATGACCTGGGCGACCTGGGGGTCATGATGTTCTGTGAAGTG
2701 CTGAAACAGCAGAGCTGCCTCCTGCAGAACCTGGGGTTGTCTGAAATGTA
2751 TTTCAATTATGAGACAAAAAGTGCGTTAGAAACACTTCAAGAAGAAAAGC
2801 CTGAGCTGACCGTCGTCTTTGAGCCTTCTTGGTAG
(SEQ ID NO:33)

FIG. 42G
65/68

1 MASTRCKLARYPTVICQEDSIEEEWMGLLEYLSRISICKMKKDYRKKYRK
 51 YVRSRFQCIEDRNARLGESVSLNKRYTRLRLIKEHRSQQEREQELLAIGK
 101 TKTCESPVSPIKMELLFDPDDEHSEPVHTVVFQGAAGIGKTI LARKMMLD
 151 WASGTLYQDRFDYLFYIHCREVSLVTQ RSLGDLIMSCCPDPNPP I HKIVR
 201 KPSRILFLMDGFDELQGA FDEHIGPLCTDWQKAERGDILLSS LIRKKLLP
 251 EASLLITTRPVALEKLQHLLDHP RHVEILGFSEAKRKEYFFKYFSDEAQA
 301 RAAFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQT SKTTTAV
 351 YVFFLSSLLQPRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNH
 401 GLQKADVSAFLRMNLFQKEVDCEKFYSFIHMTFQEFFAAMYLL EEEKEG
 451 RTNVPGSRLKLPSRDVTV LLENYGFKEGYLIFVVRFLFGLVNQERTSYL
 501 EKKLSCKISQQIRLELLKWI EVKAKAKKLQIQPSQLELFYCLYEMQEEDF
 551 VQRAMDYFPKIEINLSTRMDH MVSSFCIENCHRVESLSLGLFHNMPKEEE
 601 EEEKEGRHLD MVQC VLPSSSHAACSHGLVNSHLTSSFCRGLF SVLSTSQS
 651 LTELDSLSDNSLGD PGM RVL CETLQH PGCNIRRLWLGR CGLSHECCFDI SL
 701 VLSSNQKLVELDLS DNALGDFGIRLLCVGLKHLLCNLKKLWLVSCCLTSA
 751 CCQDLASVLSTSHSLTRLYVGENALGDSGVAILCEKAKNPQC NLQKLGLV
 801 NSGLTSVCCSALSSVLSTNQN LTHLYLRGNTLGDKG I KLLCEGLLHPDCK
 851 LQVLELDN CNLTSHCCWDLSTLLTSSQSLRKLSLGNNDLGDLGVMMFCEV
 901 LKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPELTVVFEP SW
 (SEQ ID NO:34)

FIG. 42H

1 ATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCATGGATTGGTGAACAG
 51 CCACCTCACTTCCAGTTTTTGCCGGGGCCTCTTTTCAGTTCTGAGACCA
 101 GCCAGAGTCTAACTGAATTGGACCTCAGTGACAATTCTCTGGGGGACCCA
 151 GGGATGAGAGTGTTGTGTGAAACGCTCCAGCATCCTGGCTGTAA CATTCTG
 201 GAGATTGTGGTTGGGGCGCTGTGGCCTCTCGCATGAGTGCTGCTTCGACA
 251 TCTCCTTGGTCCTCAGCAGCAACCAGAAGCTGGTGGAGCTGGACCTGAGT
 301 GACAACGCCCTCGGTGACTTCGGAATCAGACTTCTGTGTGTGGGACTGAA
 351 GCACCTGTTGTGCAATCTGAAGAAGCTCTGGTTGGTCAGCTGCTGCCTCA
 401 CATCAGCATGTTGTCAGGATCTTGCATCAGTATTGAGCACCAGCCATTCC
 451 CTGACCAGACTCTATGTGGGGGAGAATGCCTTGGGAGACTCAGGAGTCGC
 501 AATTTTATGTGAAAAAGCCAAGAATCCACAGTGTAACCTGCAGAACTGG
 551 GGTGGTGAATTCTGGCCTTACGTCAGTCTGTTGTTTCAGCTTTGTCTCTG
 601 GTACTCAGCACTAATCAGAATCTCACGCACCTTTACCTGCGAGGCAACAC
 651 TCTCGGAGACAAGGGGATCAA ACTACTCTGTGAGGGACTCTTGCA CCCCCG
 701 ACTGCAAGCTTCAGGTGTTGGAATTAGACA ACTGCAACCTCACGTCACAC
 751 TGCTGCTGGGATCTTTCCACACTTCTGACCTCCAGCCAGAGCCTGCGAAA
 801 GCTGAGCCTGGGCAACAATGACCTGGGCGACCTGGGGGT CATGATGTTCT
 851 GTGAAGTGCTGAAACAGCAGAGCTGCCTCCTGCAGAACCTGGGGTTGTCT
 901 GAAATGTATTTCAATTATGAGACAAAAAGTGCGTTAGAAACACTTCAAGA
 951 AGAAAAGCCTGAGCTGACCGTCGTCTTTGAGCCTTCTTGGTAG
 (SEQ ID NO:35)

FIG. 42I

1 MASTRCKLARYHGLVNSHLTSSFCRGLF SVLSTSQSLTELDSLSDNSLGD P
 51 GMRVLCETLQH PGCNIRRLWLGR CGLSHECCFDI SLVLSSNQKLVELDLS
 101 DNALGDFGIRLLCVGLKHLLCNLKKLWLVSCCLTSACCQDLASVLSTSHS
 151 LTRLYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSS
 201 VLSTNQN LTHLYLRGNTLGDKG I KLLCEGLLHPDCKLQVLELDN CNLTSH
 251 CCWDLSTLLTSSQSLRKLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLS
 301 EMYFNYETKSALETLQEEKPELTVVFEP SW (SEQ ID NO:36)

FIG. 42J

1 ATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCTGGAGGACCTGGAGGA
51 TGTGGACTTGAAGAAATTTAAGATGCACCTTAGAGGACTATCCTCCCCAGA
101 AGGGCTGCATCCCCCTCCCGAGGGGTCAGACAGAGAAGGCAGACCATGTG
151 GATCTAGCCACGCTAATGATCGACTTCAATGGGGAGGAGAAGGCGTGGGC
201 CATGGCCGTGTGGATCTTCGCTGCGATCAACAGGAGAGACCTTTATGAGA
251 AAGCAAAAAGAGATGAGCCGAAGTGGGGTTTCAGATAATGCACGTGTTTCG
301 AATCCCCTGTGATATGCCAGGAAGACAGCATTGAAGAGGAGTGGATGGG
351 TTTACTGGAGTACCTTTTCGAGAATCTCTATTTGTAAAATGAAGAAAGATT
401 ACCGTAAGAAGTACAGAAAGTACGTGAGAAGCAGATTCCAGTGCATTGAA
451 GACAGGAATGCCCGTCTGGGTGAGAGTGTGAGCCTCAACAAACGCTACAC
501 ACGACTGCGTCTCATCAAGGAGCACCGGAGCCAGCAGGAGAGGGAGCAGG
551 AGCTTCTGGCCATCGGCAAGACCAAGACGTGTGAGAGCCCCGTGAGTCCC
601 ATTAAGATGGAGTTGCTGTTTGACCCCGATGATGAGCATTCTGAGCCTGT
651 GCACACCGTGGTGTTCAGGGGGCGGCAGGGATTGGGAAAACAATCCTGG
701 CCAGGAAGATGATGTTGGACTGGGCGTCGGGGACACTCTACCAAGACAGG
751 TTTGACTATCTGTTCTATATCCACTGTCTGGGAGGTGAGCCTTGTGACACA
801 GAGGAGCCTGGGGGACCTGATCATGAGCTGCTGCCCCGACCCAAACCCAC
851 CCATCCACAAGATCGTGAGAAAACCCTCCAGAATCCTCTTCCTCATGGAC
901 GGCTTCGATGAGCTGCAAGGTGCCTTTGACGAGCACATAGGACCGCTCTG
951 CACTGACTGGCAGAAGGCCGAGCGGGGAGACATTCTCCTGAGCAGCCTCA
1001 TCAGAAAGAAGCTGCTTCCCGAGGCCTCTCTGCTCATCACCACGAGACCT
1051 GTGGCCCTGGAGAACTGCAGCACTTGCTGGACCATCCTCGGCATGTGGA
1101 GATCCTGGGTCTTCTCCGAGGCCAAAAGGAAAGAGTACTTCTTCAAGTACT
1151 TCTCTGATGAGGCCCAAGCCAGGGCAGCCTTCAGTCTGATTGAGGAGAAC
1201 GAGGTCTCTTCAACCATGTGCTTCATCCCCCTGGTCTGCTGGATCGTGTG
1251 CACTGGACTGAAACAGCAGATGGAGAGTGGCAAGAGCCTTGCCCAGACAT
1301 CCAAGACCACCACCGCGGTGTACGTCTTCTTCTTTCCAGTTTGCTGCAG
1351 CCCCAGGGAGGGAGCCAGGAGCACGGCCTCTGCGCCCACCTCTGGGGGCT
1401 CTGCTCTTTGGCTGCAGATGGAATCTGGAACCAGAAAATCCTGTTTGAGG
1451 AGTCCGACCTCAGGAATCATGAGACTGCAGAAGGCGGATGTGTCTGCTTTC
1501 CTGAGGATGAACCTGTTCCAAAAGGAAGTGGACTGCGAGAAGTTCTACAG
1551 CTTTCATCCACATGACTTTCCAGGAGTTCTTTGCCGCCATGTACTACCTGC
1601 TGGAAAGAGGAAAAGGAAGGAAGGACGAACGTTCCAGGGAGTTCGTTTGAAG
1651 CTTCCCAGCCGAGACGTGACAGTCTTCTGGAAAACCTATGGCAAATTCTGA
1701 AAAGGGGTATTTGATTTTTTGTGTGACGTTTCCTCTTTGGCCTGGTAAACC
1751 AGGAGAGGACCTCCTACTTGGAGAAAGAAATTAAGTTGCAAGATCTCTCAG
1801 CAAATCAGGCTGGAGCTGCTGAAATGGATTGAAGTGAAAGCCAAAGCTAA
1851 AAAGCTGCAGATCCAGCCCAGCCAGCTGGAATTGTTCTACTGTTTGTACG
1901 AGATGCAGGAGGAGGACTTCGTGCAAAGGGCCATGGACTATTTCCCCAAG
1951 ATTGAGATCAATCTCTCCACCAGAATGGACCACATGGTTTCTTCCTTTTG
2001 CATTGAGAACTGTCATCGGGTGGAGTCACTGTCCCTGGGGTTTCTCCATA
2051 ACATGCCCCAAGGAGGAAGAGGAGGAGGAGGAAAAGGAAGGCCGACACCTTGAT
2101 ATGGTGCAGTGTGTCCTCCCAAGCTCCTCTCATGCTGCCTGTTCTCATGG
2151 GTTGGGGCGCTGTGGCCTCTCGCATGAGTGCTGCTTCGACATCTCCTTGG
2201 TCCTCAGCAGCAACCAGAAGCTGGTGGAGCTGGACCTGAGTGACAACGCC
2251 CTCGGTGACTTCGGAATCAGACTTCTGTGTGTGGGACTGAAGCACCTGTT
2301 GTGCAATCTGAAGAAGCTCTGGTTGGTCAGCTGCTGCCTCACATCAGCAT
2351 GTTGTGAGGATCTTGATCAGTATTGAGCACCAGCCATTCCCTGACCAGA
2401 CTCTATGTGGGGGAGAATGCCTTGGGAGACTCAGGAGTCGCAATTTTATG
2451 TGAAAAAGCCAAGAATCCACAGTGTAACTGCAGAACTGGGGTTGGTGA
2501 ATTCTGGCCTTACGTGAGTCTGTTGTTTCAGCTTTGTCTCGGTACTCAGC

Rec'd PCT/PTO 21 OCT 2004

2551 ACTAATCAGAATCTCACGCACCTTTACCTGCGAGGCAACACTCTCGGAGA
 2601 CAAGGGGATCAAACTACTCTGTGAGGGACTCTTGCACCCCGACTGCAAGC
 2651 TTCAGGTGTTGGAATTAGACAACTGCAACCTCACGTCACTGCTGCTGG
 2701 GATCTTTCCACACTTCTGACCTCCAGCCAGAGCCTGCGAAAGCTGAGCCT
 2751 GGGCAACAATGACCTGGGCGACCTGGGGGTGATGATGTTCTGTGAAGTGC
 2801 TGAAACAGCAGAGCTGCCTCCTGCAGAACCTGGGGTTGTCTGAAATGTAT
 2851 TTCAATTATGAGACAAAAAGTGCCTTAGAAACACTTCAAGAAGAAAAGCC
 2901 TGAGCTGACCGTCGTCTTTGAGCCTTCTTGGTAG
 (SEQ ID NO:148)

FIG. 42L

1 MASTRCKLARYLEDLEDVDLKKFKMHLEDYPPQKGCIP LPRGQTEKADHV
 51 DLATLMIDFN GEEKAWAMAVWIFAAINRRDLYEKAKRDEPKWGS DNARVS
 101 NPTVICQEDSIEEEWMGLLEYLSRISICKMKKDYRK KYRKYVRSRFQCIE
 151 DRNARLGESVSLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTCESPVSP
 201 IKMELLFDPDDEHSEPVHTTVVFQGAAGIGKTI LARKMMLDWASGTL YQDR
 251 FDYLFYIHCREVSLVTQ RSLGDLIMSCCPDPNPP IHKIVRKPSRI LFLMD
 301 GFDELQGA FDEHIGPLCTDWQKAERGDILLSSLIRKKLLPEASLLITTRP
 351 VALEKLQHLLDHPRHVEILGFSEAKRKEYFFKYFSDEAQAARAAFS LIQEN
 401 EVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTSKTTTAVYVFFLSSLLQ
 451 PRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQKADVSAF
 501 LRMNLFQKEVDCEKFYSFIHMTFQEFFAAMY YLLEEEKEGRTNVPGSR LK
 551 LPSRDVTV LLENYKFKPEKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQ
 601 QIRLELLKWIEVKAKAKKLQIQPSQLELFYCLYEMQEEDFVQRAMDYFPK
 651 IEINLSTRMDH MVSSF C IENCHRVESLSLGLFHNMPKEEEEEKEGRHLD
 701 MVQCVLPSSSHAACSHGLGRGLSHECCFDI SLVLSSNQKLVELDLSDNA
 751 LGDFGIRLLCVGLKHLLCNLKKLWLVSCLTSACCQDLASV LSTSHSLTR
 801 LYVGENALGDSGVAILCEKAKNPQC NLQKLGLVNSGLTSVCCSALSSVLS
 851 TNQNLTHLYLRGNTLGDKGIKLLCEGLLHPDCKLQVLELDNCNL TSHCCW
 901 DLSTLLTSSQSLRKLSLGNNDLGDLGVMMFCEVLKQQSC LLQNLGLSEMY
 951 FNYETKSALET LQEEKPELT VVVFPSW (SEQ ID NO:149)

FIG. 42M

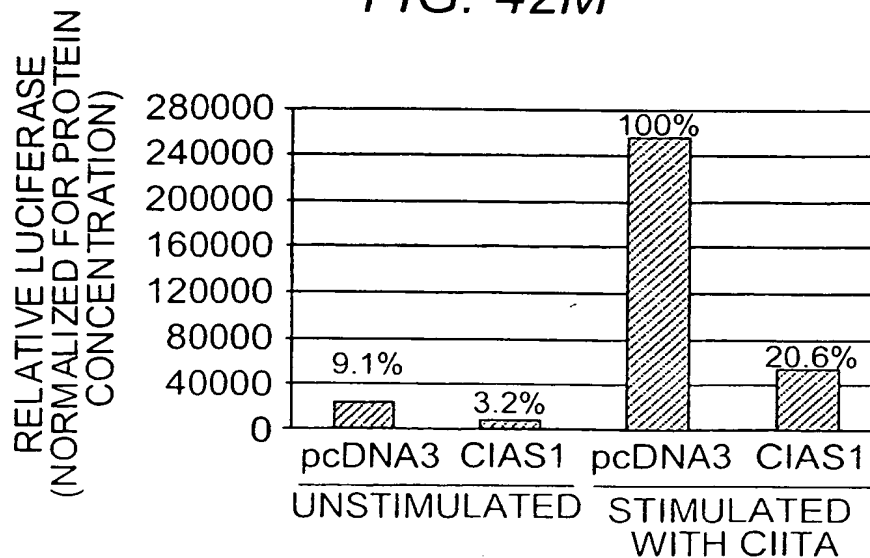


FIG. 43